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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
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Copyright (c) 1993 - 2000 Com
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US-08-97-827-10
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US-09-385-028-13
US-09-385-028-13
US-09-817-180-1
US-08-765-907A-6
US-08-765-907A-6
US-08-765-907A-7
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Sequence 1, Appli	Sequence 1, Appli	Sequence 20, Appl	Sequence 20, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 14, Appl	Sequence 14, Appl	Sequence 4, Appli	Sequence 4, Appli	•	Sequence 22, Appl	•	•	•	Sequence 23, Appl	Sequence 23, Appl	Sequence 1, Appli

## ALIGNMENTS

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RESULT 1
US-08-147-784-1
; NAME/KEY: CDS; LOCATION: 15..845; OTHER INFORMATION: US-08-147-784-1
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,784
FILING DATE: 03-NOV-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Willaim M
REGISTRATION NUMBER: 05490A-220
REFERENCE/DOCKET NUMBER: 05490A-220
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08147784 Patent No. 5821332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Godfrey, Wayne
APPLICANT: Buck, David
APPLICANT: Engleman, Edgar G.
TITLE: OF INVENTION: RECEPTOR ON THE SURFACE OF ACTIVATED
TITLE OF INVENTION: CD4+ T-CELLS: ACT-4
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                    TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 base pairs
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HYPOTHETICAL: 1
FEATURE:
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                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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STATE: California
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Best Local Similarity 99.1 Matches 1056; Conservative

99.8%;

Pred. No. 3.200; Mismatches

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; GENERAL INFOR
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APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,967
FILING DATE: 10-FEB-194
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 05490A-230
TELEFRENCE/DOCKET NUMBER: 05490A-230
TELEFRENCE/DOCKET NUMBER: 05490A-230
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TELEGRENCE/OCKET NUMBER: 05490A-230
TELEGRENCE/OCKET
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LOCATION: 15..845
OTHER INFORMATION:
US-08-195-967-1
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Best Local Similarity 99.1
Matches 1056; Conservative
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APPLICANT: Engleman, Edgar G.
TITLE OF INVENTION: LIGAND (ACT-4-L) TO A RECEPTOR ON THE SURFACE OF ACTIVATED
TITLE OF INVENTION: CD4+ T-CELLS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1020
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TYPE: nucleic acid
STRANDEDNESS: single
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tcagctccaagccgtgcaagccctgcacgtggtgtaacctcagaagtggggagtgagcgga
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99.8%;
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Pred. No. 3.2e-189;
0; Mismatches 1;
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US-08-472-940-1
                                                                                                                                 Sequence 1, Application US/08472940 Patent No. 6277962 GENERAL INFORMATION:
                                                          GENERAL INFORMATION:
APPLICANT: Godfrey, Wayne
APPLICANT: Buck, David
APPLICANT: Engleman, Edgar G.
TITLE OF INVENTION: RECEPTOR ON THE
TITLE OF INVENTION: CD4 T-CELLS: ACCUMENCES: 2
CORRESPONDENCE ADDRESS:
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 STREET: 379 Lytton
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
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                               SSEE: Townsend and Townsend F: 379 Lytton Avenue Palo Alto
                                                                                 ON THE SURFACE
ELLS: ACT-4
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                                                   Crew
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; FEATURE:
; NAME/KRY: CDS;
; LOCATION: 15..845
; OTHER INFORMATION:
US-08-472-940-1
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REFERENCE/DOCKET NUMBER: 0549
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 1056; Conserv
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,940
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US OF FILING DATE: 03-NOV-1993 ATTORNEY/AGENT INFORMATION: NAME: Smith, Willaim M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: 11
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tggacagetacaagectggagttgactgtgececetgecetecaggggagettetteecag
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Pred. No. 3.2e-189;
0; Mismatches 1;
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540 480 480 420

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US-08-192-480A-1
                                                                                     ADDRESSEE: Klarquist Sparkman Campbell
ADDRESSEE: Klarquist Sparkman Campbell
ADDRESSEE: Leigh & Whinston
STREET: 121 S. W. Salmon Street, Suite 160
STREET: 121 S. W. Salmon Street, Suite 160
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WOIGHERICATION DATA:
APPLICATION UMBER: US/08/192,480A
FILING DATE:
CLASSIFICATION UMBER: US/08/192,480A
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/192,480A
FILING DATE:
FILING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08192480A Patent No. 5759546 GENERAL INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Richard J. Polley,
REGISTRATION NUMBER: 28,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: TREATMENT OF CD4 T-CELL TITLE OF INVENTION: MEDIATED CONDITIONS NUMBER OF SEQUENCE: 3 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Andrew D. APPLICANT: Vandenbark
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Andrew D. Weinberg and Arthur A.
                 28,107
  4282-38649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suite 1600
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; MOLECULE TYPE: CDN
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRACHENT TYPE:
US-08-192-480A-1
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TELEPHONE: (503) 226-7391
TELEPAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 848 base pairs
TYPB: Nucleic acid
STRANDEDNESS: Double
TOPOLOGY: Linear
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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gaggcagtttccggacccccatccaagaggagcaggccgacgcccactccaccctggcca
                                 CCCTGTACCTGATCCGGAGGGACCAGAGGCTGCCCCCGATGCCCACAAGCCCCCTGGGG
                                               ccctgtacctgctccggagggaccagaggctgcccccgatgcccacaagccccctgggg
                                                                                                 CCGCCATCCTGGGACTGGGACTGGTGCTGGGGCTGCTGGACCCCTGGACATCCTGCTGG
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No. 7.9e-146;
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LOCATION: 1..1317;
SEQUENCE DESCRIPTION: SEQ
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US-08-097-827-10
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Best Local Similarity
                                                                                                                                                                               Matches
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FILING DATE: 23-Jul-1993
CLASSIFICATION: <UDATONNAM
ATTORNEY/AGENT INFORMATION:
NAME: Peckins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2806
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                         FEATURE
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IMMEDIATE SOURCE:
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                                                   GAGTGCCAGCCAGGCCATGGTATGGTGAACCGCTGTGATCATACCAGGGATACTCTATGT
                                                                   gagtgcaggccaggcaacgggatggtgagccgctgcagccgctcccagaacacggtgtgc 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Immunex Corporation STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1317 base pairs
                                                                                                                                                                              Conservative
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Fanslow, William
Gayle, Richard
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                                                                                                                                                                                           Score 286.6;
Pred. No. 3e
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                                                                       APPLICATION NUMBER: US/08/49
FILING DATE: 22-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/09
FILING DATE: 23-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricla
    INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Fanslow, William
APPLICANT: Gayle, Richard
TITLE OF INVENTION: No. 5783665el Cytokine Which is a Ligand
TITLE OF INVENTION: 00440
                  REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0730
                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
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STATE:
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                                             Sequence 6, Application US/08097827 GENERAL INFORMATION:
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Best Local Similarity 66.6%;
Matches 428; Conservative
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   CLONE: MOX40FC Mutein
FEATURE:
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LENGTH: 1317 base pairs
TYPE: nucleic acid
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                                    APPLICANT:
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                                                                                                                                            ctggtgctgggctgctgggccccctggccatcctgctggccc
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Fanslow, William
                                    Baum, Peter
Gayle, Richard
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Pred. No. 3e-46;
0; Mismatches 209;
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Best Local Similarity 70.6
Matches 394; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
APPLICATION NUMBER: US/08/097,827
FILING DATE: 23-Jul-1993
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
RECISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2806
TELECOMMUNICATION INFORMATION:
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LOCATION: 1..618
SEQUENCE DESCRIPTION: SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
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                                           GTTGACTGTTCCCTGCCCTCCTGGCCACTTTTCTCCAGGCAACAACCAGGCCTGCAAG
                                                       gttgactgtgccccctgccctccagggcacttcttcccaggcgacaaccaggcctgcaag
                                                                                                   ACTGTCTGCAGATGTAGACCAGGCACCCAACCTCGGCAGGACAGCGGCTACAAGCTTGGA
                                                                                                                                                            ACACAGTGCAACCATCGAAGTGGAAGTGAACTCAAGCAGAATTGCACACCTACTCAGGAT
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STRANDEDNESS: single
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Pred. No. 1.3e-45;
0; Mismatches 158;
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US-08-494-574-6
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                 Matches 394;
                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Fanslow, william APPLICANT: Gayle, Richard TITLE OF INVENTION: NO. 5783665el Cytokine Which is TITLE OF INVENTION: 0x40
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APPLICANT:
                                                                                                                                                                       MOLECULE TYPE: CE
HYPOTHETICAL: NO
ANTI-SENSE: NO
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LENGTH: 618 base pairs
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                                                                                                                                FEATURE:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                NAME: Perkins, Patricia A. REGISTRATION NUMBER: 34,693 REFERENCE/DOCKET NUMBER: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/494,574 FILING DATE: 22-JUN-1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0
FILING DATE: 23-JUL-1993
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Fanslow, William
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70.6%;
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              Score 283.2; DB 1
Pred. No. 1.3e-45;
0; Mismatches 158
                                           DB 1;
                                        Length
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US-08-911-423-3
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                                                                                                             COUNTRY: USA
ZIP: 94304-1104
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, VCURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                         CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
US
                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gorman, Daniel M. APPLICANT: Randall, Troy D. APPLICANT: Zlotnik, Albert
PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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                                                                                                                                                                                                 COUNTRY:
ZIP: 943
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                                                                    APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-AUG-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                             STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87
                          APPLICATION NUMBER: US 60/023,419 FILING DATE: .16-AUG-1996
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                                                                                                                                                                                                                                                                        DNAX Research Institute
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 US 60/027,901
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US-08-911-423-3
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Best Local Similarity
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TELEFAX: 650-496-1200
INFORMATION FOR SEQ ID NO: 3:
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REFERENCE/DOCKET NUMBER: DX
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
TELEPAX: 650-496-1200
       FILING DATA:
CLASSIFICATION: 536
CRASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 6(
APPLICATION NUMBER: US 6(
APPLICATION NUMBER: US 6(
                                                                                                                                            ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-1005
                                                                             SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/911,423 FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 07-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
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                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 8
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LOCATION: 1..723
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APPLICATION DATA:
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                                                                                                                                                                                                                                                                                   901 California Avenue
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Zlotník, Albert
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                                                                                                                                                                                                                                                                                                                                                                       MAMMALIAN CELL SURFACE ANTIGENS; RELATED
                               US 60/023,419
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; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-911-423-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO:
                                                                            APPLICATION NUMBER: US/07/
FILING DATE: 1992011
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Ribando, Curtis P
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cheung, A
APPLICANT: Wesley, R
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs
TYPE: nucleic acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 309-685-4011 ext.513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P
                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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STREET:
Peoria
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                             TELEPHONE:
                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    agcaatagctcggacgcaatctgtgaggacagggaccccccagccacgc 537
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                  309-685-4128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Andrew K.
Ronald D.
                                                                                                                                                                                                                                                                                                                                                       ; P. Ribando
5352596th University Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudorabies Virus Deletion Mutants
                                                                                                                                                                                                                                                                                                                                                                                                                                Involving The EPO and LLT Genes
                                                                                                                                                          US/07/945,283
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SEQUENCE CHARACTERISTICS: LENGTH: 8438 base pair

LENGTH: 8438 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double

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RESULT 12
US-07-959-941-1
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; LOCATION:
US-07-945-283-1
                                              Sequence 1, Application US/07959941 Patent No. 5364781 GENERAL INFORMATION:
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Best Local Similarity
Matches 181; Conserv
                        APPLICANT: APPLICANT:
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  APPLICANT:
                                                                                                                                    5196 GGGCCCGTGCCCGTCTTCATCCCG
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HUTCHINSON, Charles R.
MADDURI, Krishna M.
TORTI, Francesca
COLOMBO, Anna L.
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Pred. No. 0.24;
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US-07-959-941-1
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Best Local Similarity
Matches 187; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 16
RE
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 18-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 199210
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                                                                                                                                                                                                                                                                                                                 TGCGACTGATCCGCCACCTGGTGGCGATCGGACTGCTCGAGGAGGACGCACCGGGCGAGT
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ilarity 48.8%;
Conservative
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5 Fifteenth Street N.W.
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                                                                                                                                                                                                                                                                                              Query Match
Best Local
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ZIP: 2005-5/v.

ZIP: 2005-5/v.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: IBM PC compatible

TWOITER: IBM PC COMPATIBLE

TWO TYPEM: PC-DOS/MS-DOS
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (202)638-5000
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APPLICATION NUMBER:
FILING DATE: 09-OCT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: TORTI, Francesca
APPLICANT: COLOMBO, Anna L.
TITLE OF INVENTION: PROCESS FOR PREPARING DAUNORUBICIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: HUTCHINSON, Charles
APPLICANT: MADDURI, Krishna M.
APPLICANT: TORTI, Erancesca
APPLICANT: COLOMBO, Anna L.
                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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                                                                     340
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REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 7 FILING DATE: 18-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
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                                cctggccaagatctgaccttgggcccaccaaggtggacgctg-ggccccgccaggctgga 891
                                                                   TGCACACGCCCATGGTCGTCCGGACGGCCGCCACCCTGCGGCTCGTCGACCACATCCTGG
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DEDNESS: double
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09-OCT-1992
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Pred. No. 0.29;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for WI
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/C
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APPLICANT: Trunch, Alem
APPLICANT: Young, Peter
TITLE OF INVENTION: Tumor
TITLE OF INVENTION: TRA
                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
PRIOR APPLICATION NUMBER:
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ADDRESSEE: SmithKline
STREET: 709 Swedeland
                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION: NAME: Han, William T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                    MOLECULE TYPE:
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                                                                                                                                                                                                                                                TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: King of Prussia
ggctgagcaccgtgacggggttccactgtgtcggggacaccttaccccagcaacgaccggt 138
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                                              GCCTGTCGCTGTGCCTGGTGTTGGCGCTGCCTGCCCTGCCGGTGCCGGCTGTAC 192
                                                                   GGCACGACCTGACGCAGGCCGTGGCGCGCCGACATCTCCTTCACCCGCCTCCCCGACG 579
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                                                                                                           Conservative
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                                                                                                                         Score 47.2; DB Pred. No. 0.43;
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; TYPE: DNA
; ORGANISM: Homo sapien
US-09-286-529-18
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Patent NO. 6297367
GENERAL INFORMATION:
APPLICANT: Catherine Tribouley
TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
FILE REFERENCE: 1408.003/200130.439C1
CURRENT APPLICATION NUMBER: US/09/286,529
CURRENT FILING DATE: 199-04-05
NUMBER OF SEQ ID NOS: 25
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 4.5%;
Best Local Similarity 46.4%;
Matches 154; Conservative
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                                                                               139 gctgccacgagtgcaggccaggcaacgggatggtgagccgctgcagccgctcccagaaca 198
                                                                                                                                                                                                                                                                                                                                                         400 gcggagtggcagaaacacccacctacccctggcgggacgcagagacaggggagcggctgg 459
                                                                                                                                                                                                                                                                                                                                                                                                                               373 GCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGCACGGGCTTGCCACGCCA 432
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                                                                                                                                                  580 gccgctactgcaacgtcctctgcggggagcgtgaggaggaggcacgggcttgccacgcca
                                                                                                                                                                        259 agccctgcacgtggtgtaacctcagaagtgggagtgagcgggaagcagctgtgcacggcca 318
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                                                                                                                                                                                                                                                                                                                                                                              CGACGTGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 47.2; DB 4; Length 1347; Pred. No. 0.44; 0; Mismatches 178; Indels 0
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Result
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Maximum Match 100%
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Maximum DB
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Perfect score:
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Fas antigen precur
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C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens
C.Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
C.Accession: I3752
R.Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.;
Eur. J. Immunol. 24, 677-683, 1994
A;Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignm
A;Reference number: I37552; MUID:94170844
A;Accession: I37552
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-277 < CRESS
A;Cross-references: EMBL:X75962; NID:9472957; PIDN:CAA53576.1; PID:9472958
C;Superfamily: CD27 antigen; NGF receptor repeat homology
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## ALIGNMENTS

expression and chromosomal assignmen

Fo

RESULT 2 \$12783 \$12783 OX40 antigen precursor - rat N;Alternate names: nerve growth factor receptor homolog C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999 C;Accession: \$12783; \$08036 R;Mallett, S; Fossum, S; Barclay, A.N. EMBO J. 9, 1063-1068, 1990	OY 241 RRDQRLPPDAHKPPGGGSFRTPIQEEQADAHSTLAKI 277	Qy 181 GPPARPITVQPTEAWPRTSQGPSTRPVEVPGGRAVAAILGLGLLVLGLLGPLAILLALYLL 240 	QY 121 PGVDCAPCPPGHFSPGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPATQPQETQ 180	Qy 61 NTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDSYK 120	QY 1 MCVGARRLGRGPCAALLLLGLGLSTVTGLHCVGDTYPSNDRCCHECRPGNGMVSRCSRSQ 60	Query Match 100.0%; Score 1538; DB 2; Length 277; Best Local Similarity 100.0%; Pred. No. 5e-94; Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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gene ox40 protein - mouse

N:Alternate names: OX40 antigen

C:Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000

C;Accession: I48700; I48344; S34377

R:Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle
J. Immunol. 151, 5261-5271, 1993

A:Title: Cloning of mouse OX40: a T cell activation marker that may mediate T-B
A:Reference number: I48700; MUID:94044750

A:Reference number: I48700; MUID:94044750

A:Recession: I48700

A:Status: translated from GB/EMBL/DDBJ

A:Molecule type: mRNA
A;Residues: 1-272 <RES>
A;Cross-references: EMBL:Z21674; NID:g312827; PIDN:CAA79772.1; PID:g312828

R:Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
Eur. J. Immunol. 25, 926-930, 1995

Eur. J. Immunol. 25, 926-930, 1995

A;Reference number: I48334; MUID:95255413

A;Recession: I48334; MUID:95255413

A;Recession: I48334; MUID:95255413

A;Residues: 1-14, 'G', 16-272 <RE2>
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C;Genetics:
A;Gene: OX40
A;Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C;Superfamily: CD27 antigen; NGF receptor repeat homology
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A;Accession: $12783
A;Molecule type: mRNA
A;Residues: 1-271 <MAL>
A;Cross references: EMBL:X17037; NID:957830; PIDN:CAA34897.1;
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: growth factor receptor; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <MATS
F;20-271/Product: OX40 antigen #status predicted <MATS
F;211-235/Domain: transmembrane #status predicted <TMM>
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                     857; DB 2;
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A;Cross-references: GDB:120234; OMIM:162010
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C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprote; F;1-28/Domain: signal sequence #status predicted <SIG>
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A:Recession: A60204

A:Accession: A60204

A:Molecule type: protein

A:Residues: 29-31,'T',33-42,'TT',45-46,'TX',50-51,'XX',54-56 <MAR>
A:Residues: 29-31,'T',33-42,'TT',45-46,'TX',50-51,'XX',54-56 <MAR>
A:Experimental source: melanoma cell line A875

A:Experimental source: melanoma cell tine A875

A:E
                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M21621; NID:g189206; PIDN:AAA36363.1; PID:g189207 C;Comment: This receptor is found on sensory and sympathetic neurons, on C;Comment: The cysteine-rich region of the extracellular domain may form C;Comment: This protein is thought to form a high-affinity receptor when C;Comment: This receptor undergoes both N- and O-linked glycosylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A; Residues: 183-208 <VIS>
R; Sehgal, A; Patil, N; Chao, M.
Mol. Cell. Biol. 8, 3160-3167, 1988
Mol. Cell. Biol. 8, 3160-3167, 1988
A; Title: A constitutive promoter directs expression
A; Reference number: 157638; MOID: 89096903
A; Accession: 157638
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C;Datce: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change
C;Datce: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change
C;Accession: A25218; A60204; S21689; I57638
C;Accession: D; Lanahan, A; Buck, C.R.; Sehgal, A.; Morgan, C.;
R;Johnson, D; Lanahan, A; Buck, C.R.; Sehgal, A.; Morgan, C.;
Cell 47, 545-554, 1986
A;Tille: Expression and Structure of the human NGF receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
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                                                                                                                                                                                                                                                              C; Comment:
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-22 <RES>
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A; Status: preliminary
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J. Neurochem. 48, 225-232, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:M14764; NID:g189204; PIDN:AAB59544.1; PID:g189205 R;Marano, N.; Dietzschold, B.; Earley Jr., J.J.; Schatteman, G.; Thompson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-427 < JOH>
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phosphoprotein;

receptor

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A;Cross-references: GDB:215268; OMIM:109535
A;Map position: 20q12-20q13.2
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-27/Product: B-cell activation protein CD40 #status experimental <MAT>
F;21-193/Domain: extracellular #status predicted <EXT>
F;194-215/Domain: transmembrane #status predicted <CYT>
F;216-277/Domain: intracellular #status predicted <CYT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B-cell activation protein CD40 precursor - human N;Alternate names: B-cell surface antigen Bp50 C;Species: Homo sapiens (man) C;Date: 03-Un-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000 C;Accession: S04460; A60771
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                                                                                                                                                                                                                                                                                                                                A; Accession: A60771
A; Molecule type: protein
A; Residues: 21-50 <BRA>
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                                                                                                                                                                                                                                                       A;Experimental source:
C;Genetics:
A;Gene: GDB:CD40
                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: Biochemical characteristics and partial amino acid sequence of the receptor-lip. A; Reference number: A60771; MUID:89093941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: A B-lymphocyte activation molecule related A;Reference number: S04460; MUID:89356608 A;Accession: S04460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Immunol. 142, 562-567, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X60592; NID:g29850; PIDN:CAA43045.1; R;Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-277 <STA>
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F;153,180/Binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGAGATGRAMDGPRILLILLIGVSIGGAKEACPTGL-----YTHSGECCKACNIGEGVA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGVVTTVMGSSQPVVTRGTTDNLIPVYCSILAAVVVGLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLAGKHTLQPASNSSDAICED------RDPPATQPQETQGPPARPITVQPTE 193
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site: carbohydrate (Asn)
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Pred. No. 8.4e-08;
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(covalent) #status
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stroem, P.;
predicted
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A; Referen A; Reseren A; Status: A; Molecul A; Residue A; Cross-r A; Note: S; R; Heller, Proc. Nat A; Referen A; Accessi	A; Status: pp A; Molecule A; Residues: A; Cross-reff A; Cross-reff A; Cross-reff A; Cross-reff A; Cross-reff A; Reference A; Reference A; Reference A; Recession A; Status: pp A; Molecule A; Residues: A; Cross-reff A; Dembic, Z Cytokine Z A; Title: Tw	RESULT A35356 tumor C, Pate C, Date C, Date C, Rosnit Scienci	Db Oy		Query M Best Lo Matches Qy 26 Db 15
ence number: A48416; MUID:91370690  sion: A48416 s: preliminary s: preliminary ule type: mRNA; protein ues: 23-461 < DEM> -references: GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649 -references: GB:S63368; NID:g235649 -references: GB:S63368	A; Rctatus: preliminary A; Rolocule type: mRNA A; Residues: 1-461 <smi> A; Residues: 1-461 <smi> A; Residues: 1-461 <smi> A; Residues: 1-461 <smi> A; Residues: 1-461 <smi 1-155,="" 1-461="" 197-461="" 1990="" 8331-8335,="" 87,="" <koh="" <smi="" a="" a36475;="" a;="" acad.="" baker,="" can="" factor="" gene="" hale,="" k.k.;="" king,="" kr,="" m.w.;="" molecule="" mrna="" muid:91045991="" natl.="" naturally="" necrosis="" number:="" oc="" p.e.;="" preliminary="" proc.="" product="" receptor="" reference="" residues:="" ritle:="" s.l.;="" schwartz,="" sci.="" second="" shed="" squir="" tumor="" type:="" u.s.a.=""> A; Residues: 1-155, Kr, 197-461 <koh> A; Coss-references: GB:M55994; GB:M38549; NID:9339757; PIDN:AAA36755.1; PID:9339758 R:Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, Cytokine 2, 231-237, 1990 A; Title: Two human TNF receptors have similar extracellular, but distinct intracellul</koh></smi></smi></smi></smi></smi>	RESULT 6 A35356 A36266; A36266	175 OPQETQGPPARPITVQPTEAWPRTSQEPSTRVEVPGGRAVAAILGLGLVLGLLGPLAIL 234  187	P-CKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDSYKPGVD	y Match 14.4%; Score 221.5; DB 2; Length 277; Local Similarity 23.2%; pred. No. 9.1e-08; hes 66; Conservative 34; Mismatches 95; Indels 89; Gaps 10; 26 VTGLHCVGDTYPSNDRCCHECRPGNGMVSRCSRSONTVCRPCGPGFYNDVVSSK 79 1

A:Status: preliminary
A:Molecule type: mRNA
A:ROLecule type: mRNA
A:Residues: 116-140,'P',142-195,'R',197-362,'T',364-461 <HEL>
A:Cross-references: GB:M35857; NID:g339751; PIDN:AAA63262.1; PID:g339752
R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, J. Biol. Chem. 265, 20131-20138, 1990

Purification and partial amino acid sequence analysis of two distinct tumor

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A; Molecule type: protein
A; Residues: 23-40;55-69;136-141;300-306 < LOE>
A; Residues: 23-40;55-69;136-141;300-306 < LOE>
A; Residues: 23-40;55-69;136-141; D.
J. Biol. Chem. 265, 1331-1356, 1990
A; Title: Two tumor necrosis factor-binding proteins purified from human urine. A; Reference number: A35010; MUID:90110215
A; Recession: B35010
A; Status: preliminary
A; Molecule type: protein
A; Molecule type: pr
                                                                                                                                   RESULT
A26431
nerve growth factor receptor precursor, 1
%Alternate names: NGF receptor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10
C;Accession: A26431; PH1229
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A; Accession: A23666
A; Status: preliminary
A; Molecule type: protein
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Best Local S
Matches 74
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                                                                                                                                                                                                                                                                                                                                                                                                      PWTNCTLAGKHTLQPASNSSDAICEDRDPPATQPQETQGPPA----RPITV--QPTEAWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AKVFCTKTSDTVCDSCEDSTYTQLWNWVP--ECLSCGSRCSSDQVETQACTREQNRICTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MVSRCSRSQNTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSER--KQLCTATQDTVCRC
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                                                                                                                                                                                                                                                                                                                                                       PHQICNVVA----IPGNASMDAVC----TSTSPTRSMAPGAVHLPQPVSTRSQHTQPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RAG------TQPLDSYKPG------VDCAPCPPGHFS--PGDNQACK
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                                                                                                                                                                                                                                                                                                  ----PVEVPGGRAVAAILGLGLVLGL--LGPLAI
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Pred.
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                         10-Sep-1999 #text_change 10-Sep-1999
                                                                                                            low
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No. 2
                                                                                                       affinity
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.8e-07;
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R; Large, T.H.; Weskamp, G.; Helder, J Neuron 2, 1123-1134, 1989 A; Title: Structure and developmental A; Reference number: JN0006; MUID:9016 A; Accession: JN0006

MUID: 90166579

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J.С.;

Radeke,

M.J.; Misko,

T.P.; Shooter,

E.M.,

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10-Sep-1999 #text\_change 10-Sep-1999

chicker

nerve growth factor receptor, low affinity precursor • N;Alternate names: NGF receptor C;Species: Gallus gallus (chicken)

C;Date: 10-Sep-1999 #sequence\_revision C;Accession: JN0006; A60504

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C; Superfamily: nerve growth factor receptor; NGF receptor repe
C; Superfamily: nerve growth factor receptor; NGF receptor repe
C; Superfamily: nerve growth factor receptor factors; F; 129/Domain: signal sequence #status predicted <SIG>
F; 30-425/Product: nerve growth factor receptor #status predict
F; 30-251/Domain: NGF receptor repeat homology <NG1>
F; 33-66/Domain: NGF receptor repeat homology <NG3>
F; 110-148/Domain: NGF receptor repeat homology <NG3>
F; 110-148/Domain: NGF receptor repeat homology <NG3>
F; 150-190/Domain: NGF receptor repeat homology <NG4>
F; 252-273/Domain: transmembrane #status predicted <NEM>
F; 252-273/Domain: transmembrane #status predicted <NEM>
F; 274-425/Domain: intracellular #status predicted <NEM>
F; 274-425/Domain: intracellular #status predicted <NEM>
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A;Cross-references: GB:X61269
C;Comment: This receptor is found on sensory and sympathetic neurons, on C;Comment: The cysteine-rich region of the extracellular domain may form C;Comment: This protein is thought to form a high-affinity receptor when C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Cross-references: GB:X05137; NID:g56755; PIDN:CAA28783.1; PID:g56756 R;Metsis, M.; Timmusk, T.; Allikmets, R.; Saarma, M.; Persson, H. Gene 121, 247-254, 1992
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A; Residues: 1-425 < RAI
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VADMVTTVMGSSQPVVTRGTTDNLIPVYCSILAAVVVGLV
                                                                                                                                                                             AYGYYQDEETGHCEACSVCEVGSGLVFSCQDKQNTVCEECPEGTYSDEANHVDPCLPCTV 170
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                                                                                                                                                                                                                                                                                                                                                                                                          RRLGRGPCAA-----LLLLGLGLST-----VTGLHCVGDTYPSNDRCCHECRPGNGM 52
                                        EAWPRTSQGPSTRPVE-----VPGGRAVAAILGLGLV
                                                                                       CE-DTERQLRECTPWADAECEEIPGRWIPRSTPPEGSDSTAPSTQEPEVPPEQDL-VPST
                                                                                                                             CTLAGKHTLQPASNSSDAICED----
                                                                                                                                                                                                                                                                       AQPCGANQ-TVCEPCLDNVTFSDVVSATEPCKPCTECLGLQSMSAP---CVEADDAVCRC
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C; Superfamily: tumor necrosis factor receptor type 1;

NGF receptor repeat homology

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R; Baens, M.; Chaffanet, M.; Cassiman, J.J. Genomics 16, 214-218, 1993
A; Title: Construction and evaluation of a A; Reference number: 154182; MUID:93252381
A; Accession: 154182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma of:Comment: The cysteine-rich region of the extracellular domain may form part or all of C:Comment: This protein is thought to form a high-affinity receptor when it associates of C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; the comment of the cysterior of the cysterio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision
C;Accession: I54182
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F;21-416/Product: nerve growth factor receptor *status predicted <MAT>
F;21-239/Domain: extracellular *status predicted <EXT>
F;24-57/Domain: NGF receptor repeat homology <NG1>
F;59-100/Domain: NGF receptor repeat homology <NG2>
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A; Cross-references: A; Map position: 12pl
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F;262-416/Domain:
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A; Residues: 1-416 < LAR>
                                                                                A; Gene: GDB: LTBR
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12p13.3-12p13.1
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A;Note: sequence extracted from NCBI backbone (NCBIP:120357) C;Comment: For an alternative splice form, see PIR:A46515. C;Comment: For an alternative splice form, see PIR:A46476. C;Superfamily: CD27 antigen; NGF receptor repeat homology C;Keywords: alternative splicing; transmembrane protein F;105-144/Domain: NGF receptor repeat homology <NGF>
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                                                                                                                                                                                                                                                                                                                               A;Molecule type: nucleic acid
A;Residues: 1-287,'LV' <GRI>-
A;Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059;
A;Experimental source: BALB/C, liver
                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Genomic structure and chromosomal mapping of A;Reference number: A46515; MUID:93094586 A;Accession: A46515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:M83312; NID:g1553058
A;Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIP:75207)
A;Note: this translation is not annotated in GenBank entry MUSCD40A, releas
R;Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard,
J. Immunol. 149, 3921-3926, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A46476; A; Accession: A46476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Differential increase of an alternatively polyadenylated A;Reference number: A46476; MUID:92105763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B cell-associated surface molecule CD40, long splice C;Species: Mus musculus (house mouse) C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #t C;Accession: A46476; A46515
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                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; not compared with conceptual translation
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                                                                                                                                      Query Match
Best Local
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                                                                             VTGLH----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KQLCTATQDTVCRCRAG----
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-PCKPCTWCNLRSGSERKQLCTATQDTVCRCRAG
                                    LTAVHLGQCVTCSDKQYLHDGQCCDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCKN---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCRPCDPVMGLEE
                                                                                                               64;
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67; Conser
                                                                                                                                    Similarity
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                                                                         -CVGDTYPSNDRCCHECRPGNGMVSRCSRSQNTVCRPCGPGFYNDVVSSK 79
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22.0%;
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No. 8.
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                                                                                                                                      209; DB 2;
No. 6.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281
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                                                                                                                                                      Length 305;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the murine CD40 gene
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RESULT 12
B38634
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                                                                                                                                                                                                                                         망
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A:Molecule type: DNA
A:Residues: 1-256 <RES>
A:Cross-references: EMBL:U02567; NID:g1117783; PIDN:AAA93113.1;
C:Genetics:
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A:Title: Genomic Organization and Chromosomal Localization of A:Reference number: I48879; MUID:94179805
A:Accession: I48879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A32393; MUID:89184547
A; Accession: B32393
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Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967,
A:Title: cDNA sequence of two inducible T-ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 21-Jul-2000
C;Accession: B3239; 14887.
R;Kwon, B.S.; Weissman, S.M.
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A; Residues: 1-256 <KWO>
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                                                                                                                                                                                                                                                                                                                                                                                                 CDNCQPGT----FCRKYNPVCKSCPPSTFSSIGGQPNCNICRVC---AGYFRFKKFCSS
                                                                                                                                                                                                                                                                                                                                                                                                                                   CHECRPGNGMVSRCSRSQNTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSER-KQLCTA 101
                                                                                   DACSCRCPQEEE
                                                                                                                   GGGSFRTPIQEE
                                                                                                                                                            --PGGHSLQVLTLFLALTSALLLALIFITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQEE
                                                                                                                                                                                                EVPGGRAVAAI-LGLGLVLGLLGPLAILLALY-LLRRDQRLPPDAHKPP-----
                                                                                                                                                                                                                                           SLDGRSVLKTGTTEKDVVC--
                                                                                                                                                                                                                                                                               TLAGKHTLQPASNSSDAICEDRDPPATQPQETQGPPARPITVQPTEAWPRTSQGPSTRPV
                                                                                                                                                                                                                                                                                                                      THNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTCSLGTFNDQNGTGVCRPWTNC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                     266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.2%; Score 202.5; DB 2 25.4%; Pred. No. 1.5e-06;
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C;Accession: I48854
R;Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A;Title: Allelic variation of the type 2 tumor necrosis
A;Reference number: I48854; MUID:95178848

factor

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gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1
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A;Residues: 1-22 <KIS>
A;Residues: 1-22 <KIS>
A;Residues: 1-22 <KIS>
A;Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044
A;Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat P;1-22/Domain: signal sequence #status predicted <SIG>
F;1-22/Domain: NGF receptor repeat homology <NG1>
F;40-77/Domain: NGF receptor repeat homology <NG2>
F;166-203/Domain: NGF receptor repeat homology <NG4>
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C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: B38634; A40254; S54816
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.;
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis A;Accession: B38634; MUID:91187885
A;Accession: B38634
A;Molecule type: mRNA
A;Molecule type: mRNA
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C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992
C:Accession: B38634; A40254: S54816
                                                                                    RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Molecular cloning and expression A;Reference number: A40254; MUID:91246168 A;Accession: A40254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-474 <LEW>
A; Residues: 1-474 <LEW>
A; Cross-references: GB: M60469; NID: g199827; PIDN: AAA39752.1; PID: g199828
R; Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Cope.
Mol. Cell. Biol. 11, 3020-3026, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
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A; Residues: 1-474 <GOO>
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Best Local Similarity 25.1
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                                                                                                                                                                                              MLGLVNCIILVQRKKKPSCLQRDAKVPHVPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAKCPPGQYVKHFCNKTSDTVCADCEASMYTQVWNQ--FRTCLSCSSSCTTDQVEIRAC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCHECRPGNGMYSRCSRSQNTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQL--C
                                                                                                                                                                                                                                                                                                                                                  PARPITYOPTEAWPRTSOGPS-----TRPV---EVPGGRAVAAILGLGLVLGLLGPLAI 233
                                                                                                                                                                                                                                                                                                                                                                                                           SDTTSSTDVCRPHRICSILA----IPGNASTDAVCAPESPTLSAIPRTLYVSQPEPTRS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                         S--PGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDP-----PAT----QPQETQGP 182
                                                                                                                                                                                                                                                                                                 QPLDQEPGPSQTPSILTSLGSTPIIEQSTKGG
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Pred. No. 2.5e-06;
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A; Molecule type: mRNA
A; Residues: 1-106, 'R', 108-255 <SCH>
A; Residues: 1-106, 'R', 108-255 <SCH>
A; Residues: 1-106, 'R', 108-255 <SCH>
C; Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-necrd C; Comment: This receptor recongnizes soluble, cell-surface bound or extracellular matrix C; Superfamily: CD27 antigen; NGF receptor repeat homology
C; Keywords: glycoprotein; phosphoprotein; receptor: transmembrane protein
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-255/Product: lymphocyte activation-induced receptor ILA #status predicted <MAT>
F;187-213/Domain: transmembrane #status predicted <TMM>
F;187-213/Domain: transmembrane #status predicted <TMM>
F;187-213/Binding site: carbohydrate (Asn) (covalent) (by casein kinase C) #status predicted
F;242/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:U03397; NID:g571320; PIDN:AAA53133.1; PID:g571321 R;Schwarz, H.; Tuckwell, J.; Lotz, M. Gene 134, 295-298, 1993 Gene 134, 295-298, 1993 A;Title: A receptor induced by lymphocyte activation (ILA): a new member of the A;Reference number: JT0752; MUID:94085794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lymphocyte activation-induced receptor ILA precursor - human c;Species: Homo sapiens (man) C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 01-Dec-2000 C;Accession: I38426; JT0752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Molecular and biological characterization of human 4-1BB and its ligand. A;Reference number: I38426; MUID:94374434
A;Accession: I38426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Alderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, Eur. J. Immunol. 24, 2219-2227, 1994
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-459 <RES>
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A; Residues: 1-255 < RES>
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Best Local
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CHECRPGNGMVSRCSRSQNTVCRPCGPGFYNDVVSSKPCKPCTWCN--LRSGSERKQLCT 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KQQNRVCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTFS 157
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                                                                                       Similarity
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Pred. No. 2.9e-06;
34; Mismatches 89;
                                                    Score 186.5; DB 2
Pred. No. 1.7e-05;
5; Mismatches 108
                                                                                                              DB 2;
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Que Bes Mat	RESULT GORTT1 tumor UN; Cont- C; Spec C; Date C; Acces R; Himm DNA Ce A; Titl, A; Refe A; Titl, A; Resi A; Resi A; Cross C; Compe C; Supe C; Supe C; Supe C; Supe F; 30-4 F; 30-2 F; 168- F; 168- F; 168- F; 231- F; 125- F; 158- F; 231-	04 04 04 04 04 04 04 04 04 04 04 04 04 0
Query Match 11.2%; Score 172; DB 1; Length 461; Best Local Similarity 23.7%; Pred. No. 0.00025;	RESULT 15 GQRTT1 tumor necrosis factor receptor 1 precursor - rat N; Contains: tumor necrosis factor binding protein 1 (TNF blocking factor) C; Species: Rattus norvegicus (Norway rat) C; Date: 30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change 22-Jun-1999 C; Accession: B36555 R; Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M DNA Cell Biol. 9, 705-715, 1990 A; Title: Molecular cloning and expression of human and rat tumor necrosis factor rece A; Reference number: A36555; MUID:91090841 A; Accession: B36555 A; Molecula type: mRNA A; Residues: 1-461 <him> A; Cross-references: GB:MG3122; NID:9207361; PIDN:AAA42256.1; PID:9207362 C; Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) C; Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology C; Keywords: duplication; glycoprotein; receptor; transmembrane protein F; 30-461/Product: tumor necrosis factor receptor type 1 *status predicted <mat> F; 30-201/Product: tumor necrosis factor binding protein *status predicted <mat> F; 44-82/Domain: NGF receptor repeat homology <ng1> F; 44-82/Domain: NGF receptor repeat homology <ng2> F; 168-204/Domain: KGF receptor repeat homology <ng3> F; 168-204/Domain: transmembrane *status predicted <mem> F; 235-461/Domain: transmembrane *status predicted <mem> F; 235-461/Domain: normain: Normain *status predicted <mem> F; 235-461/Domain: normain *status predicted <mem> F; 235-461/Domain *status predicted <mem> F; 235-461/Domain</mem></mem></mem></mem></mem></mem></mem></mem></mem></mem></mem></mem></mem></mem></mem></mem></ng3></ng2></ng1></mat></mat></him>	28 CSNCPAGTECDNNRNQICSPCPPNSFSSAGGQRTCDICROCKGVFRTRKECS 79  101 ATQDTVCRCRAGTQPLDSYKPGVDCAPCPPGHFSPGDNQACKPWTNC 147  11

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TR1A_PIG
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Pfam; PF00020; TNFR_c6; 3.

ProDom; PD000771; TNFR_c6; 1.

SMART; SM00208; TNFR; 3.

PROSITE; PS00652; TNFR_NGFR_1; 3.

PROSITE; PS50050; TNFR_NGFR_2; 2.

Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
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LMA5_MOUSE	LMA3_HUMAN	PCK5_BRACL	T10B_HUMAN	TNR6_PIG	LMB2_RAT	TR12_HUMAN	LMB2_HUMAN	LMA1_HUMAN	LMG3_HUMAN	TR1A_BOVIN	TNR7_MOUSE
Q61001 mus musculu									Q9y6n6 homo sapien		

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P43489; Q13663; 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor superfamily member 4 precursor (OX40L receptor) (ACT35 antigen) (TAX-transcriptionally activated glycoprotein 1 receptor) (CD134 antigen).
TNFRSF4 OR TXGP1L.
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE-94170844; PubMed-7510240;

Latza U., Duerkop H., Schnittger S., Ring

"Hummel M., Fonatsch C., Stein H.;

"The human OX40 homolog: cDNA structure,

assignment of the ACT35 antigen.";

Eur. J. Immunol. 24:677-683(1994).
EMBL; X75962; CAA53
EMBL; S76792; AAB33
HSSP; P25942; 1CDF.
                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=95219871; PubMed=7704935;
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                          CAA53576.1;
AAB33944.1;
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M.R.;
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use by
                                                                    Mallett S., Fossum S., Barclay A.N.;
"Characterization of the MrC OX40 antigen of activa lymphocytes -- a molecule related to nerve growth f EMBO J. 9:1063-1068(1990).

-- FUNCTION: RECEPTOR FOR THE DAVAOL/GP34 CYTOKINE.

-- SUBCELLULAR LOCATION: Type I membrane protein.

-- TISSUE SPECIFICITY: ACTIVATED T-CELLS.

-- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
                                                                                                                                                                                                                                                       01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor superfamily member receptor) (OX40 antigen) (MRC OX40).
TNFRSF4 OR TXGPIL OR OX40.
Rattus norvegicus (Rat)
                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                      MEDLINE-90214614; PubMed-2157591;
                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                     NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGVDCAPCPPGHFSPGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPATQPQETQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDSYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MCVGARRLGRGPCAALLLLGLGLSTVTGLHCVGDTYPSNDRCCHECRPGNGMVSRCSRSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPPARPITVQPTEAWPRTSQGPSTRPVEVPGGRAVAAILGLGLVLGLLGPLAILLALYLL
                                                                                                                                                                                                                                                                                                                                                                                                                   RRDQRLPPDAHKPPGGGSFRTPIQEEQADAHSTLAKI
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277; Conserv
  non-profit
and this st
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ilarity 100.0%;
Conservative
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215
236
30
66
108
127
  statement
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235
277
277
107
126
167
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             institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.

TUMOR NECROSIS FACTOR RECEPTOR
SUPERPAMILY MEMBER 4.

EXTRACELLULAR (POTENTIAL).
POTENTIAL.

CYTOPLASMIC (POTENTIAL).
TIMER-CYS 1.
TIMER-CYS 3.
TIMER-CYS 3 (INCOMPLETE).
TIMER-CYS 3 (INCOMPLETE).
TIMER-CYS 4.

N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
  18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1538; DB 1; Pred. No. 4.1e-99; Mismatches 0;
                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
  not
  removed.
            There are no restrictions ng as its content is in
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e growth facto
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  λq
                                                                                                                                                                                                                                                                                           precursor (OX40L
                                                                                                                                  CD4 positive '
  and
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RESULT 3
TINA4_MOUSE
ID TINA4_M
AC P47741
AC 01-FEB
DT 01-FEB
DT 16-OCT
DE TOMOT
DE TOMOT
DE TOMOT
OC Eukary
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OC Mammal
ON NCBI_T
RN [1]
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Best Local Sin
Matches 168;
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TRANSMEM
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REPEAT
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CARBOHYD
SEQUENCE
                                                                                                  TNR4_MOUSE STANDARD: PRT; 2:
P47741;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Tumor necrosis factor receptor superfa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SMUUZUO, INT., NGER_1; 3.

PROSITE; PS00652; TNFR_NGER_2; 2.

PROSITE; PS50050; TNFR_NGER_2; 2.
STRAIN=BALB/C;
MEDLINE=94044750;
Calderhead D.M., I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro: IPR001368; TNFR_c6. pfam; PF00020; TNFR_c6; 3. proDom; PD000071; TNFR_c6; 1. smarr; SM00208; TNFR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S08036; S08036.
PIR; S12783; S12783.
HSSP; P19438; 1EXT.
                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID-10090;
                                                                        receptor) (OX40 antigen).
TNFRSF4 OR TXGP1 OR OX40.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                    253
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                                                                                                                                                                                                  PCWGNSFRTPIQEEQTDTHFTLAKI
                                                                                                                                                                                                                   PPGGGSFRTPTQEEQADAHSTLAKI
                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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211
236
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61
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124
143
271
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235
271
60
102
123
123
164
143
29895
 Buhlmann
         PubMed=8228223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19
271
                                                     Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                56.2%;
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 J.E.,
                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                                  Score 864.5; 1
Pred. No. 6.5e
18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
TNER-CYS 1.
TNER-CYS 3.
TNER-CYS 3 (INCOMPLETE).
TNER-CYS 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (F
C06465136B16E821 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 4.
                                                      Craniata; Ver
Sciurognathi;
                                                                                                      superfamily
 van
 den
                                                                                                                      update)
                                                                                                                                                     272
                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                 Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                      5; DB 1;
5.5e-53;
nes 74;
 Eertwegh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane; Repeat;
                                                                                                                                                     ξ
                                                                                                      member
                                                       Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                      precursor (0X40L
                                                       Murinae;
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                                                        Mus
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Best Local
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REPEAT
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CARBOHYD
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                              Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00020; TNFR_c6; 3. ProDom; PD000771; TNFR_c6; SMART; SM00208; TNFR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P19438; 1EXT.
MGD; MGI:104512; Tnfrsf4.
InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of rat OX40 protein.";
Eur. J. Immunol. 25:926-930(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; 221674; CAA79772.1;
EMBL; X85214; CAA59476.1;
HSSP; P19438; 1EXT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Birkeland M.L.,
Barclay A.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning
T-B cell
                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claassen
                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00652; PROSITE; PS50050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Gene structure and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=95255413;
                            190
                                                                 130
         252
                                              192
                                                                                   132
                                                                                                                        74
                                                                                                                                            10
                                                                                                                                                              15
                                                                                                     70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
                                                                                                                                                     ALLLLGLGLS-TVTGLHCVGDTYPSNDRCCHECRPGNGMVSRCSRSQNTVCRPCGPGFYN 73
                                                                                                               HFSPGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPATQPQETQGPPARPITVQP
                                                                                                    EAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVCRCRPGTQPRQDSGYKLGVDCVPCPPG
                                                                                                                                          ALLLLALTLGVTARRLNCVKHTYPSGHKCCRECQPGHGMVSRCDHTRDTLCHPCETGFYN
       KPPGGGSFRTPIQEEQADAHSTLAKI
                                                               HFSPGNNQACKPWTNCTLSGKQTRHPASDSLDAVCEDRSLLATLLWETQRPTFRPTTVQS
                                                                                                                                                                                 169;
                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interactions.";
ol. 151:5261-5271(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               f mouse 0x40: 7
                                                                                                                                                                                                                              20
212
237
26
62
104
125
144
15
272
                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; PubMed=7737295;
Copeland N.G., Gilbert D.J.,
                                                                                                                                                                                                                                                                                                                                                              TNFR_NGFR_1; 3.
TNFR_NGFR_2; 2.
Antigen; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                     TNFR_c6; 1.
                                                                                                                                                                                                                                                 211
236
272
61
103
124
144
                                                                                                                                                                                                                                                                                                                                    19
272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosomal localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R.J.,
                                                                                                                                                                                                                                30153
                                                                                                                                                                                         55.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a T cell activation
                                                                                                                                                                                                                                W.
                                                                                                                                                                                 20;
                                                                                                                                                                                                                            POTENTIAL.

CYTOPLASMIC (POTENTIAL).

TNER-CYS 1.

TNER-CYS 2.

TNER-CYS 3 (INCOMPLETE).

TNER-CYS 4.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-S GIN REF. 2).

N-S GIN REF. 2).
                                                                                                                                                                                        Score
Pred.
                                                                                                                                                                                                                                                                                                                           TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 4.
                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                 Mismatches
                                                                                                                                                                                         No. 2.
                                                                                                                                                                          DB 1
2.1e-52;
71;
                                                                                                                                                                                                                                                                                                                                                                Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOKINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      marker that may mediate
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                                                                                                                                                                                                                                               · · ) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                  Length
                                                                                                                                                                                 Indels
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                                                                                                                                                                                                    272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homologue
                                                                                                                                                                                6
                                                                                                                                                                               Gaps
                                                                                                                                           69
                                             251
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                                                                                                                        131
                                                                189
                           246
                                                                                                                                                                                4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
TNR3_MOUSE
밁
                                                                                                    DOMAIN
TRANSMEM
                                                                                                                                                   PROSITE;
                                                                                 DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Force W.R., Walter B.N., Hession Browning J.L., Ware C.F.;
                                                                                                                                                                     InterPro: IPRO01368; TNFR_c6.
pfam; PF00020; TNFR_c6; 3.
ProDom; PD000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 3.
                                                                                                                                                                                                                   EMBL; U29173; AAA68964.1; -.
EMBL; L38423; AAB00846.1; -.
EMBL; U30798; AAA81334.1; -.
HSSP; P25942; ICDF.
                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96163885;
Nakamura T., Tash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=CVB; TISSUE-Lung;
MEDLINE=96072804; PubMed=7594541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1996 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996
                                                                                                                       CHAIN
                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                   or send an
                                                                                                                                                                                                                                                                             entities requires
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lymphotoxin-beta receptor precursor LTBR OR TNFCR OR TNFRSF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P50284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TNR3_MOUSE
                                                                         REPEAT
                                                                                                                                           Receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                              Honjo T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Mouse lymphotoxin-beta receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 KPCWGNSFRTPIQEEHTDAHFTLAKI 272
                                                                                                                                                                                                                                                                                                                                          IMMUNE DEVELOPMENT.
SUBCELLULAR LOCATION: Type I men
SIMILARITY: CONTAINS 4 THER-CYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression.";
Immunol. 155:5280-5288(1995).
                                                                                                                                                                                                           MGI:104875; Ltbr.
                                                                                                                                                    PS50050;
                                                                                                                                                             PS00652;
                                                                                                                                           Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                        Tashiro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34,
40,
                                                                                                                                                  TNFR_NGFR_1;
TNFR_NGFR_2;
                                                                                                                                                                                                                                                                             ល
                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=8586432;
iro K., Nazarea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way the content is the content of the content is the content of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                email to license@isb-sib.ch).
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TNFR-CYS 3.
TNFR-CYS 4.
TNFR-CYS 4.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                             CYTOPLASMIC TNFR-CYS 1.
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Anderson D.M., Maraskovsky E., Billingsley W.L., Do
Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F.,
Galibert L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TR11_HUMAN STANDARD; PRT; 616 AA. 09Y606; 09Y606; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Tumor necrosis factor receptor superfamily member 11A precursor (Receptor activator of NF-KB) (Osteoclast differentiation factor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor) (ODFR).
TNFRSF11A OR RANK.
Homo sapiens (Human).
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Kinosaki M., Yamaguc
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Nat. Genet. 24:45-48(2000).
-!- FUNCTION: RECEPTOR FOR RANK LIGAND (ROSTEOCLAST DIFFERENTIATION FACTOR OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hughes A.E., Ralston S.F
Wallace R.G.H., van Hul
                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                           use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anderson D.M.;
Anderson D.M.;
"Mutations in TNFRSF11A, affecting
"Mutations in TNFRSF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                differentiation factor
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                                                                                                                                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                    DISEASE: DEFECTS IN TNFRSF11A ARE A CAUSE OF FAMILIAL PAGET DISEASE OF BONE, ALSO KNOWN AS PAGET DISEASE OF BONE 2 (PDB2). IT IS A BONE REMODELLING DISCADER MITH CLIMICAL SIMILARITIES TO FEO. UNLIKE FEO, HOWEVER, AFFECTED INDIVIDUALS HAVE INVOLVEMENT OF THE AXIAL SKELETON WITH LESTONS IN THE SPINE, PELVIS AND SKULL. SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
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GIAND.

DISEASE: DEFECTS IN THERSELLA ARE THE CAUSE OF EAMILIAL EXPLOISEASE: DEFECTS IN THERSELLA DOMINANT BONE DISCREER OSTEDLYSIS (PEO), A RARE AUTOSOMAL DOMINANT BONE REMODELLING.

CHARACTERIZED BY FOCAL AREAS OF INCREASED BONE REMODELLING.

CSTEDLYTIC LESIONS DEVELOP USUALLY IN THE LONG BONES DURING ADULTHOOD. FEO IS OFTEN ASSOCIATED WITH EARLY ONSET DEAFNESS

LOSS OF DENTITION.
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SUBGELLULAR LOCATION: Type I membrane protein (Potential).
TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEVELS SKELETAL MUSCLE, THYMUS, LIVER, COLON, SMALL INTESTINE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-L--L-21 DUPL,
AAB86809.1;
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Hul W., Whyte
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mmun. 253:395-400(1998).
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Nakatsuka K., Hovy
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EMBL; AF018253; AAB8 HSSP; P25942; 1CDF. MIM; 603499; -. MIM; 174810; -. MIM; 602080; -. REPEAT
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CARBOHYD DOMAIN REPEAT REPEAT Disease SIGNAL Pfam; PF00020; TNFR\_c6; 4. ProDom; PD000771; TNFR\_c6; 1. SMART; SM00208; TNFR; 4. DOMAIN CHAIN TRANSMEM PROSITE; PROSITE; nterPro; mutation PS00652; TNFR\_NGFR\_1; PS50050; TNFR\_NGFR\_2; IPR001368; TNFR\_c6 Glycoprotein; 30 213 234 71 114 1154 154 150 71 1154 1154 1154 1154 1154 212 233 616 616 112 1151 151 151 151 151 174 Transmembrane; TNER-CYS
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BY SIMILA TNFR-CYS TUMOR NECROSIS FACTOR RECE SUPERFAMILY MEMBER 11A. EXTRACELLULAR (POTENTIAL). POTENTIAL.
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01-AUG-1988 (Rel. 0
01-AUG-1988 (Rel. 0
16-OCT-2001 (Rel. 4
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16-OCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor superfamily member 16 precursor affinity nerve growth factor receptor) (NGF receptor) (Gp80-LNC (P75 ICD) (Low affinity neurotrophin receptor p75NTR).
                                                                                                                                                                                                                      "A constitutive promoter directs expression receptor gene.";
Mol. Cell ""."
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                    between
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Sehgal A., Patil N.,
                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-22 FROM N.A.
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                                                            SUBUNIT: CAN FORM A HOMODIMER THROUGH DISULFIDE B
INTERACTS WITH PY5NTR-ASSOCIATED CELL DEATH EXECU
SUBCELLULAR LOCATION: Type I membrane protein.
PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED
SIMILARITY: CONTAINS 4 THER-CYS REPEATS.
SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                              . Cell. Biol. 8:3160-3167(1988).
FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIAND NT-4. CAN MEDIATE CELL SURVIVAL AS WELL
                                                                                                                                                                    NEURAL CELLS.
                   SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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   Bioinformatics Institute.
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an A., Buck C.R.,
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LLCALL -> LLCALLLLCALL (IN FEO).
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(Gp80-LNGFR)
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 ne EMBL outstation restrictions on it
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TRANSMEM
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PROSITE;
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00531; death; 1.
Pfam; PF00020; TNFR_c6; 4.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M14764; AAB59544.1; -. EMBL; M21621; AAA36363.1; -. PIR; A25218; GQHUN. HSSP; P07174; 1NGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phosphorylation; Signal; Apoptosis SIGNAL 1 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed.
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AGVVTTVMGSSQPVVTRGTTDNLIPVYCSILAAVVVGLV
                                    AWPRTSQGPSTRPVE----
                                                                                             TLAGKHTLQPASNSSDAICED---
                                                                                                                                                                                                                      QPCGANQ-TVCEPCLDSVTFSDVVSATEPCKPCTECVGLQSMSAP---CVEADDAVCRCA
                                                                                                                                                                                                                                                                                              MGAGATGRAMDGPRLLLLLLLGVSLGGAKEACPTGL-----YTHSGECCKACNLGEGVA
                                                                                                                                             YGYYQDETTGRCEACRVCEAGSGLVFSCQDKQNTVCEECPDGTYSDEANHVDPCLPCTVC
                                                                                                                                                                                                                                                                                                                                                                     84;
                                                                        DTERQLRECTRWADAECEEIPGRWITRSTPPEGSDSTAPSTQEPEAPPEQDL-IASTV
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PS50050; TNFR_NGFR_2;
PS50017; DEATH_DOMAIN;
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30.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               MW;
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BY SIMILARITY.
                                    -VPGGRAVAAILGLGLV
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Pred. No. 7.
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nes 95;
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RESULT 7
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beard D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,
RA Huckle E., Hunt A.R., Hunt S.E., Jakosch K., Johnson C.M., Johnson D.,
RA Huckle E., Hunt A.R., Hunt S.E., Jakosch K., Johnson C.M., Johnson D.,
RA Hummond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Milliams S.M., Peck A.I.,
RA Milley S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA Swann M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wallis J.M.,
RA Wiltehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Milme S.J., Waray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1992
01-MAY-1992
01-MAR-2002
                                                                                                                                                                                                                                                                                        "The role of polar interactions with its receptor CD40."; Protein Sci. 7:1124-1135(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Construction and analysis of a contraction and analysis of a contraction of the proteins 27:59-70(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                     3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
MEDLINE-98266353; PubMed-9605317;
Singh J., Garber E., van Vlijmen H., Karpsusas M., Hsu Y.-M.,
Zheng Z., Naismith J.H., Thomas D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE-9935608; PubMed=2475341;
Stamenkovic I., Clark E.A., Seed B.;
Stamenkovic I., Clark E.A., Seed B.;
"A B-lymphocyte activation molecule related factor receptor and induced by cytokines in EMBO J. 8:1403-1410(1989).
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97189482; PubMed=9037712;
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                          FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS OF THE CONTROL OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE CARCINO OF THE CONTROL OF THE CONTRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA sequence and comparative analysis of human re 414:865-871(2001).
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etazoa; Chordata;
theria; Primates;
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he human B
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                                                                                                                                                                    protein.
IMARY CARCINOMAS
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                                                                                                                                                                                                                                                KNOWN AS CD40L
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)) (CDw40).
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REPEAT
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PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Event the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00020; TNFR_C6; 4. ProDom; PD000771; TNFR_C6; 1. SMART; SM00208; TNFR; 4.
                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00652; TNFR_NGFR_1; PROSITE; PS50050; TNFR_NGFR_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
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1CDF; 01-APR-97.
                                          LVLVFIKKVAKKPTNKAPHPKQEPQEINFPDDLPGSNTAAPVQE
                                                                                                                                                                                  P-CKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLD-----SYKPGVD----
                                                                                                                                                                                                      LTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETECLPCGESEFLDTWNRE
                                                                                                                                                                                                                           VTGLH-----CVGDTYPSNDRCCHECRPGNGMVSRCSRSQNTVCRPCGPGFYNDVVSSK
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                                                             LALYLLRRDQRLP----PDAHKPP-----GGGSFRTPIQE
                                                                                                    QPQETQGPPARPITVQPTEAWPRTSQGPSTRPVEVPGGRAVAAILGLGLVLGLLGPLAIL
                                                                                                                        ATGVSDTICEPCPVGFFSNVSSAFEKCHPWTSCETKDLVVQQAGTNKTDVVC-----
                                                                                                                                                               THCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACESCVLHRSCSPGFGVKQI 134
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                                                                                                                                                                                                                                               66;
                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B-cell; Glycoprotein;
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                                                                                                                                                                                                                                               Conservative
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194
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CYTOPLASMIC
TNFR-CYS 1.
TNFR-CYS 2.
                                                                                                                                                                                                                                                       Score 221.5;
Pred. No. 8.
                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. . .) (P
N-LINKED (GLCNAC. . .) (P
; BC8776EC2C4A5680 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        TNFR-CYS
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SUPERFAMILY MEMBER 5.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 -
                                                                                Transmembrane;
                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                            8.7e-09;
hes 95;
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                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat;
                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                               Indels
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16-OCT-2001 (Rel. 40, L
01-MAR-2002 (Rel. 41, L
Tumor necrosis factor r
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DISULFID
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Biochem. Biophys. Res. Commun. 253:395-400(1998).

-I- FUNCTION: RECEPTOR FOR RANK LIGAND (RANKL; ALSO KNOWN AS OSTEOCLAST DIFFERENTIATION FACTOR OR ODF), ESSENTIAL FOR MEDIATED OSTEOCLASTOGENESIS. INVOLVED IN THE REGULATION
                                                                                                                                                                                                                               DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mammalia; Eutheria;
                                                                                                                                                                                      DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00020; TNFR_c6; 3. ProDom; PD000771; TNFR_c6; 1. SMART; SM00208; TNFR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nakagawa N., Kinosaki M., Yamaguchi K., Shima
Morinaga T., Higashio K.;
"RANK is the essential signaling receptor for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A homologue of the TNF receptor and dendritic-cell function."; Nature 390:175-179(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Receptor activator receptor) (ODFR).
TNFRSF11A OR RANK.
  DISULFID
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                                                                                                                                                                                                                                                                                                                                                       PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF019046; AAB86810.1; HSSP; P25942; 1CDF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERACTIONS BETWEEN T-CELLS AND DENDRITIC CELLS.
SUBCELULIAR LOCATION: Type I membrane protein (Potential).
TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEVELS
TRABECULIAR BONE, THYMUS, SWALL INTESTINE, LUNG, BRAIN AND K
WEAKLY EXPRESSED IN SPLEEN AND BONE MARROW.
SIMILARITY: CONTAINS 4 THER-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                       PS50050;
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TNFR_NGFR_2; 1.
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Rodentia;

    Created)
    Last sequence update)
    Last annotation update)
    receptor superfamily member 11A precursor of NF-KB) (Osteoclast differentiation factor

                                                                                                                                                                                                                                                                                                                                    Transmembrane;
                                                                                                                                                                   CYTOPLASMIC TNFR-CYS 1. TNFR-CYS 2.
TNFR-CYS
BY SIMILA
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EXTRACELLULAR
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Sciurognathi; Muridae;
Y SIMILARITY.
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                                                                                                                                                                                                         (POTENTIAL)
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Best Local
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Lepaslier D., sum
Brodeur G.M.;
Brodeur G.M.;
"Physical mapping and geno
"mins 35:94-100(1996).
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P20333;
01-FEB-1991 (Rel. 1
01-AUG-1991 (Rel. 1
16-OCT-2001 (Rel. 4
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CARBOHYD
CARBOHYD
SEQUENCE
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16-OCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor 2 precursor
binding protein 2) (TBPII) (p80) (TNF-R2) (
TNFRSFIB OR TNFR2 OR TNFBR.
                                                                                                                                                                                                                                                                               Smith C.A., Davis T., Anderson Dower S.K., Cosman D., Goodwin "A receptor for tumor necrosis cellular and viral proteins."; Science 248:1019-1023(1990).
                                                                                                                                                                                     Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.; "A second tumor necrosis factor receptor gene product naturally occurring tumor necrosis factor inhibitor."; proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=91045991;
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=90260639;
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                and
                                              SEQUENCE OF 116-461 FROM N.A., AND MEDLINE=90349572; PubMed=2166946; Heller R.A., Song K., Onasch M.A.,
                                                                                                                               MEDLINE=96299745; PubMed=8661109; Beltinger C.P., White P.S., Maris J. Lepaslier D., Stallard B.J., Goeddel
                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                      Ringold G.M
                                                                                                                                                                  SEQUENCE
                          "Complementary
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   y DNA cloning of
tion of a shed fo
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y; PubMed=2160731;
T., Anderson D., Solam
Goodwin R.G.;
Goodwin factor defines ar
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                                                                                                         genomic
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of a receptor for tumor d form of the receptor.";
..A. 87:6151-6155(1990).
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Pred. No. 1.8e
17; Mismatches
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N-LINKED (GLCNAC. . .) (P

N-LINKED (GLCNAC. . .) (P

F8C1872E99511D8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                         Craniata; V
Catarrhini;
                                                                                                         structure
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No. 1.8e-08;
                                                  Fischer
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                                                                         PARTIAL
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                                                                                                                                                                                                                                                                                                                                                                                        Vertebrata;
i; Hominidae;
                                                                                                         of
                                                                                                                                           Sulman
                           for tumor necrosis
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                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. Thuse by non-profit institutions as long modified and this statement is not removed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Blochemical properties of the 75-kDa tumor necrosion of ligand binding, internalization, characterization of ligand binding, internalization, characterization.";
                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem.
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SEQUENCE OF 27-31.
MEDLINE=90110215; PubMed=2153136;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Purification and partial amino acid sequence distinct tumor necrosis factor receptors from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHARMACEUTICAL: Available under the name Enbrel (Immunex and Wyeth-Ayerst). Used to treat moderate to servere rheumatoid arthritis (RA). Enbrel consist of the extracellular ligand-binding portion of TNFR2 linked to an Immuglobulin Fc chain. It binds to TNF-alpha and blocks its interactions with receptors. SIMILARTY: CONTAINS 4 TWRR-CYS REPEATS.

SIMILARTY: CONTAINS 4 TWRR-CYS REPEATS.

DATABASE: NAME-PROW; NOTE-CD guide CD120b entry;
WHW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd120b.htm".

DATABASE: NAME-Enbrel; NOTE-CLInical information on Enbrel;
WHW-"http://www.enbrelinfo.com/".
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                  M32315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through the Swiss Institute of Bioinformatics and the Ex
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Lam V.T., Mize N.K., Weber
Goeddel D.V.;
                                        A35356.
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AAA63262.1;
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A23666; A23666.
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26.0%;
Last sequence update)
Last annotation update;
receptor superfamily member 16 precursor (Low-
factor receptor) (NGF receptor) (Gp80-LNGFR)
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-> T (IN REF. 4).
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EMBL; X61269; -; NOT_ANNO
PIR; A26431; A26431.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature
[2]
                                                                                                                                                                                                                                        PDB; 1NGR; 29-JUL-97.
InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_c6
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-I- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAND NT-4. CAN MEDIATE CELL SURVIVAL AS NEURAL CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=87115859; PubMed=3027580;
Raddake M.J., Misko T.P., Hsu C., Herr
"Gene transfer and molecular cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                           the
                                                                REPEAT
                                                                                                                                        SIGNAL
                                                                                                                                               Phosphory.
                                                                                                                                                         Receptor;
                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                               tities requires a license agreement (See send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: CAN FORM A HOMODIMER THROUGH DISULFIDE I SUBCELLULAR LOCATION: Type I membrane protein. PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED SIMILARITY: CONTAINS 4 THER-CYS REPEATS. SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                       s SWISS-PROT entry is copyright. It is produced ween the Swiss Institute of Bioinformatics and European Bioinformatics Institute. There are a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ICD)
                                                                                                                                                                                                                                                                                                                                                 γď
                                                                                                                                                                                                PF00531; death; 1.
PF00020; TNFR_c6; 4.
; SM00005; DEATH; 1.
; SM00208; TNFR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                325:593-597(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D) (Low affinity neurotrophin receptor p75NTR).
TNFRSF16.
                                                                                                                                                                 PS00652; TNFR_NGFR_1; 3
PS50050; TNFR_NGFR_2; 4
PS50017; DEATH_DOMAIN;
                                                                                                                                                                                                                                                                                                                          non-profit instituted and this statement requires a license
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                                                                                                                                               lation;
                                                                                                                                                         Neurogenesis;
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                                                                                                                                                                                                                                                                                                                                              institutions as long as its content
                                                                                                                                                        Transmembrane;
                                                                                                                                               Apoptosis;
                                                  POTENTIAL.
CYTOPLASMIC (
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
                                                                                                                                                                                                                                                                                                                                    is not removed.
TNFR-CYS 4.
DEATH.
SER/THR-RICH.
BY SIMILARITY
BY SIMILARITY
                                                                                                     TUMOR NECROSIS FACTOR SUPERFAMILY MEMBER 16 EXTRACELLULAR (POTENT
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Sciurognathi;
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ning of the
                                                                                                                                               3D-structure
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                                                                                  (POTENTIAL)
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p75
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                                                                                                      (POTENTIAL).
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rat nerve growth factor
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                                                                                                                                                                                                                                                                                                                                   Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neurotrophin receptor.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor promoter.";
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; Murinae; Rat
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P18519;
01-NOV-1990 (Rel. 16, C
01-NOV-1990 (Rel. 16, I
16-OCT-2001 (Rel. 40, I
                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor necrosis factor receptor superfamily member 16 paffinity nerve growth factor receptor) (NGF receptor) (P75 ICD) (Low affinity neurotrophin receptor p75NTR). NGFR OR TNERSF16.
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CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
Archosauria; Aves; Neogn
                                                                                                                                                               "Structure and developmental expression receptor in the chicken central nervous Neuron 2:1123-1134(1989).
                                                                                                                                                                                                                            Large T.H., Weskamp G., Helde. Shooter E.M., Reichardt L.F.;
                                                                                                                                                                                                                                                                  MEDLINE=90166579; PubMed=2560385;
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                                                                                                                                                                                                                                                                                         TISSUE=Brain;
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; Galliformes; Phasianidae; Phasianinae;
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No. 3e-08;
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SEQUENCE OF 21-416 FROM N.A.

MEDLINE-90152140; Pubmed-2154393;
Heuer J.G., Fatemie-Nainie S., Wheeler I
"Structure and developmental expression
Dev. Biol. 137:287-304(1990).
-i- FUNCTION: LOW AFFINITY RECEPTOR WHIC

n of t

the chicken NG

NGF

receptor.";

NT-4.

AFFINITY RECEPTOR WHICH CAN BIND MEDIATE CELL SURVIVAL AS WELL AS

TO NGF, BDN

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Pfam; PF00720; TNFR_C6; 4.

SMART; SM00005; DEATH; 1.

SMART; SM00208; TNFR; 3.

PR0SITE; PS00652; TNFR_NGFR_1; 3.

PROSITE; PS50050; TNFR_NGFR_2; 3.

PROSITE; PS50017; DEATH_DOMAIN; 1.

Receptor; Neuroganesis; Transmembrane; Gl
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SIGNAL 1
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PIR; A60504; A60504.
HSSP; P07174; INGR.
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SUBUNIT: CAN FORM A HOMODIMER THROUGH DISULFIDE BOND FORMATION.

SUBCELLULAR LOCATION: Type I membrane protein.

PYM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.

SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

SIMILARITY: CONTAINS 1 DEATH DOMAIN.
     PGGRAVAAILGL
                                                                                                      GLMFPCRDSQDTVCEECPEGTFSDEANFVDPCLPCTICE - ENEVMVKECTATSDAECRDL
                                                                                                                                                                         TVSATEPCKPCTQCVGLHSMSAP---CVESDDAVCRCAYGYFQDELSGSCKECSICEVGF
                                                                                                                                                                                                      VVS-SKPCKPCTWC-NLRSGSERKQLCTATQDTVCRCRAG---TQPLDSYK-----
                                                                                                                                                                                                                                                                           LLLLGLGLSTVTGLHCVGDTYPSNDRCCHECRPGNGMVSRCSRSQNTVCRPCGPGF-YND
                                      HPRWTTHTPSLAGSDSPEPITRDPFNTEGMATTLADIVTTVMGSSQPVVSRGTADNLIPV
                                                                                                                                                                                                                                           LLLLPAGPTWGSKEKCLTKMYTTSGECCKACNLGEGVVQPCGVNQ-TVCEPCLDSVTYSD
                                                                                                                                                                                                                                                                                                             l Similarity
77; Conser
                                                                                                                                         PGVD----
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                               ۶Ą,
                                                                                                                                                                                                                                                                                                                                                                                          Signal;
                                                                                                                         -CAPCPPGHFSPGDN--QACKPWTNCTLAGKHTLQPASNSSDAICEDR
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30
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                                                                                                                                                                                                                                                                                                                                                                                               MW;
                                                                                                                                                                                                                                                                                                             23;
                                                                                                                                                                                                                                                                                                                                                                                          DEATH.

SER/THH-RICH.
BY SIMILARITY.
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SUPERFAMILY MEME
EXTRACELLULAR (E
POTENTIAL.
CYTOPLASMIC (POT
TNER-CYS 1.
                                                                                                                                                                                                                                                                                                             Score 211.5;
Pred. No. 6e-0
23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNFR-CYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNFR-CYS
                                                                                                                                                                                                                                                                                                                           211.5; DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein;
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                                                                                                                                                                                                                                                                                                                                              DB
                                                                                                                                                                                                                                                                                                             101;
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                                                                                                                                                                                                                                                                                                                                                                                               CRC64;
                                                                  -AWPRTSOGPSTRPVEV
                                                                                                                                                                                                                                                                                                                                         Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat;
                                                                                                                                                                                                                                                                                                                                              416;
                                                                                                                                                                                                                                                                                                             51;
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                       169
                                                                                                                                                                         124
                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                           74
                                      243
                                                                    209
                                                                                                      183
                                                                                                                                                                                                                                                                                                             13;
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TD TNR3_HUMAN
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                                                                                                                                                                                                                                                                                                    PROSITE; PS50050; TNFR_C6; 4.

SMART; SM00208; TNFR, 26; 1.

PROSITE; PS00652; TNFR_NGFR_1; PROSITE; PS50050; TNFR_NGFR_1;
                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L04270;
HSSP; P25942;
MIM; 600979;
 REPEAT
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                                                                                                                                                                                                      TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                           Receptor;
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94225209; PubMed=8171323;
Crowe P.D., van Arsdale T.L., Walter B.N
Ehrenfels B., Browning J.L., Din W.S., G.
"A lymphotoxin-beta-specific receptor.";
Science 264:707-710(1994).
-!- FUNCTION: RECEPTOR FOR THE LYMPHOTOX
IMMUNE DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Construction and evaluation of a hncDNA library of human 12p transcribed sequences derived from a somatic cell hybrid."; Genomics 16:214-218(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lymphotoxin-beta receptor precursor 2 related protein) (Tumor necrosis : LTBR OR TNFCR OR TNFRSF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P36941;
                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Liver;
MEDLINE-93252381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                       REPEAT
                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001368; TNFR_c6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Type I membrane protein SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a centre S_{
m W} is Institute of Bioinformatics and the EMBL
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                                                                                                                                                                                                                                                                                           Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=8171323;
walter B.N., Ware rsdale T.L., Walter B.N., Ware wining J.L., Din W.S., Goodwin
                                                                                                                                                                                                                                                                                                             TNFR_NGFR_1; 2:
TNFR_NGFR_2; 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=8486360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             255
   Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              license agreement (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOR THE LYMPHOTOXIN-BETA.
                                                                                                                                                                                                                                                                         Glycoprotein;
POTENTIAL.
                                                                                                                                    POTENTIAL.
CYTOPLASMIC
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                         LYMPHOTOXIN-BETA
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                                                                                                                                                                                                                                                                                           Repeat;
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Matches 67
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DISULFID
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                             01-AUG-1992 (Rel. 23, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor superfamily memb
Tumor necrosis factor receptor annotation (B-cell surface antigen CD40)
                                                                                                        SEQUENCE FROM N.A.
STRAIN=BALB/C; TISSUE=Liver;
STRAIN=93094586; PubMed=1281194;
MEDLINE=93094586; PubMed=1281194;
                                                                                                                                                                                                                      "Differential increase of an a species of murine CD40 upon B J. Immunol. 148:620-626(1992).
                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                    P27512;
01-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                     MOUSE
                      This
                                                                                              Grimaldi J.C., Torres R., Kozak Howard M., Cockayne D.A.;
                                                                                                                                                                            Torres
           between
                                                                                                                                                                   Submitted (SEP-1996)
                                                                                                                                                                                       STRAIN-BALB/C;
                                                                                                                                                                                                  REVISIONS
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=92105763;
                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                           INR5_MOUSE
                                                                                   ioward M., Cockayne D.A.;
'Genomic structure and chromosomal mapping
                                                                                                                                                        Ξ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37
                                                                            Immunol.
                                         SUBCELLULAR LOCATION: Type I membrane prosimilarity: CONTAINS 4 THER-CYS REPEATS.
                                                                FUNCTION:
          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IAPCTSKRKTQCRCQPGMFCAAWALECTHCELLSDCPPGTEAELKDEVGKGNNHCVPCKA
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                                                                                                                                                                            R.M.;
                                                                                                                                                                                                                                                       R.M., Clark E.A.
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170
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177
                                                                149:3921-3926(1992).
N: RECEPTOR FOR A CYTOKINE
Bioinformatics
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185
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Sciurognathi;
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No. 8.6e-08;
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                                                                LIGAND
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thi; Muridae;
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restrictions
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EMBL; M94126; AAA37404.1;
EMBL; M94129; AAA37404.1;
EMBL; M94128; AAA37404.1;
                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
REPEAT
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Pfam; PF00020; TNFR_c6; 4.
ProDom; PD000771; TNFR.c6; 1.
SMART; SM00208; TNFR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD;
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SIGNAL
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204
                 227
                                    187
                                                       167
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                                                                                                               75
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                                                                                                                                                     15
                                                                                                                                                                       26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , M94128; AAA37404.1;
, M94127; AAA37404.1;
A46476; A46476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGI:88336; Tnfrsf5
IL--ITIFGVFLYIKKVVKKPKDNEMLPPAARRQDPQEMEDYPGHNTAAPV
                 LLGPLAILLALYLLRRDQRLPPDAHKPPGGGSFRTPIQEEQADAHSTLAKI
                                                                                                                                                                      VTGLH-----CVGDTYPSNDRCCHECRPGNGMVSRCSRSQNTVCRPCGPGFYNDVVSSK
                                                                          ATETTDTV---
                                                                                                               IRCHQHRHCEPNQGLRVKKEGTAESDTVCTCKEGQHCTSKDCEACAQHTPCIPGFGVMEM
                                                                                                                                                    LTAVHLGQCVTCSDKQYLHDGQCCDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNRE
                                                       EDRDPPATQPQETQGPPARPITVQPTEAWPRTSQGPSTRPVEVPGGRAVAAILGLGLVLG
                                                                                            -TQPLDSYKPGVDCAPCPPGHFSPGDNQA · · · - - CKPWTNCTLAGKHTLQPASNSSDAIC
                                                                                                                                - PCKPCTWCNLRSGSERKQLCTATQDTVCRCRAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P25942;
                                                                                                                                                                                          64;
                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             ; PS00652;
                                                                                                                                                                                                                                                                                                                                                                                                                                   B-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        email to
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194
216
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61
104
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                                                                         --CHPCPVGFFS--
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                           TNFR_NGFR_1; 1.
TNFR_NGFR_2; 4.
                                                                                                                                                                                                                                                            193
215
289
289
103
1144
187
37
51
59
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119
116
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32111
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                                                                                                                                                                                          39;
                                                                                                                                                                                                                                       TNFR-CYS 4.
BY SIMILARITY.
C791CB6D2FEA574E C
                                                                                                                                                                                         Score 209; DB
Pred. No. 6.5e
99; Mismatches
                                                                                                                                                                                                                                                                                                                                              TNFR-CYS
                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
CYTOPLASMIC (POTENTIAL).
TNFR-CYS 1.
                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                        SUPERFAMILY MEMBER
                                                                                                                                                                                                                                                                                                                                                                                                                TUMOR NECROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                          NOSSLFEKCYPWTSCEDKNLEVLQKGTSQTNVIC
                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (See
                                                                                                                                                                                                   DB 1;
.5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . Usage by and for commercial http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                 FACTOR
                                                                                                                                                                                          96;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Repeat; Signal.
                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                         CRC64;
                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                  (POTENTIAL)
                                     MRALLVIPVV
                                                                                                                                                                                                             289;
                  277
252
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                                     돐
                                                                                                                                                                                          Gaps
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                                     203
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RESULT 14
TNR9\_MOUSE
ID TNR9\_M
AC P20334
DT 01-FEB
DT 01-FEB

STANDARD;

256

A

TNR9\_MOUSE P20334; 01-FEB-1991 01-FEB-1991

(Rel.

17, Created)
17, Last sequence

update)

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CARBOHYD
CARBOHYD
SEQUENCE
                                              REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor superfamily memb
ligand receptor) (T-cell antigen 4-188) (CD137
TNERSE9 OR ILA OR LX63 OR CD137 OR CD157.
                                                                                                                                                                                                                                                   EMBL; J04492; AAA40167.1;
EMBL; U02567; AAA93113.1;
PIR; B32393; B32393.
                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                function.";
J. Immunol. 150:771-781(1993).
-I- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kwon B.S., Kozak C.A., Kim "Genomic organization and cantigen 4-18B.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-89184547; PubMed-2784565;
                                     REPEAT
                                                                       REPEAT
                                                                                             TRANSMEM
                                                                                                                                  CHAIN
                                                                                                                                                                                          Pfam; PF00020; TNFR_c6; SMART; SM00208; TNFR; 2.
                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                between
                                                                                                                                                                                                                                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARACTERIZATION, AND SEQUENCE OF 25-29. MEDLINE=93139510; PubMed=7678621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "cDNA sequences of two inducible T-cell genes.";
Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
Eukaryota; Metazoa; C
                                                                                     DOMAIN
                                                                                                         DOMAIN
                                                                                                                                              SIGNAL
                                                                                                                                                                                                                  MGD; MGI:1101059; Tnfrsf9.
InterPro; IPR001368; TNFR_c6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kwon B.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pollok K.E., Kim Y.-J., Zhou Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-94179805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
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W
On
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Rodentia;
                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Inducible T cell antigen 4-188. Analysis of expression
                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunol. 152:2256-2262(1994).
                                                                                                                                                                                                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Type I membrane pr
TISSUE SPECIFICITY: EXPRESSED ON THE SUR
INDUCTION: OPTIMAL BY PMA AND IONOMYCIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTIVE DURING T CELL ACTIVATION. SUBUNIT: PRINCIPALLY AN HOMODIMER,
                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: CONTAINS 4 THER-CYS REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                ASSOCIATES WITH P56-LCK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B.S., Weissman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences of two
                                                                                                                                                                 PS50050; TNFR_NGFR_1;
                                                                                                                                                        Glycoprotein;
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188
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                                                                                                                                                        Repeat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           K.K.,
                                                                  TUMOR NECROSIS FACTOR RECEP'
SUPERFAMILY MEMBER 9.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
TNER-CYS 1.
       TNER-CYS 2.
TNER-CYS 3.
TNER-CYS 4.
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                  1.
FALSE_NEG
 93A10D03C60813C4 CRC64;
                                                                                                                                                        Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hurtado J., Kin K.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pickard
                                                                                                                                 NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ard R.T.;
localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BUT
                                                                                                                                                        Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                        e protein.
SURFACE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALSO FOUND
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0137 antigen).
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                                                                                                                                                                                                                                                                                                                           by and
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Best Local
                                                                                                                                                                                                                                                                                                              necrosis specific.
                                                                                                                                                                                                                                                                                                                                      Wong G.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 P25119; p97893;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor 2 precursor (TINFRSF1B OR TNFR-2.
                                                                                          Kissonerghis M., Fellowes R., Submitted (MAY-1995) to the El
                                                                                                                                                                                                                               Goodwin R.G., Anderson D., Jerzy R., Dav. Copeland N.G., Jenkins N.A., Smith C.A.; "Molecular cloning and expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOUSE

    -i- FUNCTION: RECEPTOR FOR TNF-ALPHA.
    -i- SUBCELLULAR LOCATION: Type I membrane pr
    -i- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

                                                                                                                                                 Jacob C.O.,
Submitted (
                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                      between
                                                                                                                  TISSUE-Liver;
                                                                                                                            SEQUENCE OF 1-22 FROM
                                                                                                                                                                      STRAIN-NOD;
                                                                                                                                                                                  SEQUENCE OF
                                                                                                                                                                                                                    receptors
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=91246168; PubMed=1645445;
                                                                                                                                                                                                                                                                                                                                                             Lewis
                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-91187885; PubMed-1849278;
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43
          s SWISS-PROT entry is copyright. It ween the Swiss Institute of Bioinfo European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLAGKHTLQPASNSSDAICEDRDPPATQPQETQGPPARPITVQPTEAWPRTSQGPSTRPV
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                                                                                                                                                                                                                                                                                                                                               M., Tartaglia L.A., Lee
3.H., Chen E.Y., Goeddel
                                                                                                                                                                                                                                                                                                   Natl. Acad. Sci. U.S.A. 88:2830-2834(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 25.4
                                                                                                                                                                                                                                                                                                                                      and expression of cDNAs for two
                                                                                                                                                                                                                                                                                                                         factor receptors demonstrate
                                                                                                                                                 ., Liu J.;
(JAN-1996)
                                                                                                                                                                                                                     for tumor
                                                                                                                                                                                                           Biol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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Rodentia;
                                                                                                                                                                                                                     necrosis
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                                                                                          es R., Feldmann M., Che
the EMBL/GenBank/DDBJ
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                                                                                                                                                   the
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Pred.
                                                                                                                                                                                                                    factor.";
                                                                                                                                                                                                                                                                                                                                                 D.V.
                                                                                                                                                                                                                                                                                                                                                                                                                   Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 precursor (TNF-R2)
                    ght. It is produced through Bioinformatics and the EN
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No. 1.6
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                                                                                                                                                                                                                                                                                                                          one
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            There are no restrictions
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                                                                                                                                                                                                                                                                                                                                      distinct murine tumor
                                                                                                                                                                                                                                type 1 and
                                                                                                                                                                                                                                                                                                                         receptor
                                                                                                                                                                                                                                                                                                                                                            G.L.,
                                                                    protein
                                                                                                       Chernajovsky
                                                                                                                                                                                                                                                                                                                                                                                                                    Muridae;
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                                                                                           databases
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                         EMBL
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                         a collaboration
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                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M60469; AAA39752.1; -.
EMBL; M59378; AAA40463.1; -.
EMBL; U39488; AAA85021.1; -.
EMBL; X87128; CAA60618.1; -.
PIR; B38634; B38634.
HSSP; P19438; 1NCF.
                                                                                                                                                                                                                                                                                       CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                        CHAIN
DOMAIN
TRANSMEM
DOMAIN
REPEAT
REPEAT
REPEAT
REPEAT
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 4.
ProDom; PD00071; TNFR_c6; 1.
SMART; SM00208; TNFR_v6; 1.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 3.
Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:1314883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                 134
                                                                                                                                                              100
276
                                                                    183
                                                                                          172
                     54
                                                                                                                                                                                                          42
                                                                                                                                                                                 CCAKCPPGQYVKHFCNKTSDTVCADCEASMYTQVWNQ--FRTCLSCSSSCTTDQVEIRAC
                                                                                                                                                                                               CCHECRPGNGMVSRCSRSQNTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQL--C
                                                                  PARPITVQPTEAWPRTSQGPS-----TRPV---EVPGGRAVAAILGLGLVLGLLGPLAI 233
                                                                                                      TKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTF
                                                                                                                                                           TATQDTVCRCRAG-----TQPLDSYKPG-----VDCAPCPPGHF 133
MLGLVNCIILVQRKKKPSCLQRDAKVPHVPD
                                                                                         SDTTSSTDVCRPHRICSILA----IPGNASTDAVCAPESPTLSAIPRTLYVSQPEPTRS-
                                            -----QPLDQEPGPSQTPSILTSLGSTPIIEQSTKGGIS----LPIGLIVGVTSLGLL
                                                                                                                                                                                                                               68; Conservative
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23
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                                                                                                                                                                                                                                                                                       119 B
127 B
145 B
163 B
181 B
181 N
181 N
195 N
195 N
                                                                                                                                                                                                                              13.2%; Score 202.5; DB 1; 25.1%; Pred. No. 2.8e-07; Live 36; Mismatches 86;
                                                                                                                                                                                                                                                                                     TNER-CYS 4.

BY SIMILARITY.

OPTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNFR-CYS
TNFR-CYS
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306
                                                                                                                                                                                                                                                    Length 474;
                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                               81;
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                                                                                                                                                                                                                               Gaps
                                                                                                                182
                                                                                                                                     171
                                                                                                                                                                                   111
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                                            275
                                                                                          226
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Search completed: June 18, 2002, 14:28:29 Job time: 223 sec

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
            924
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1: sp_archea:*
2: sp_bacteria
3: sp_fung1:*
4: sp_inverteb
6: sp_mammal:*
5: sp_inverteb
6: sp_mage:*
11: sp_rodent:
12: sp_virus:*
13: sp_vartebr
14: sp_unclass
15: sp_bacteri
16: sp_bacteri
17: sp_archeap
                                                                                                                                                                                                      Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   June 18, 2002, 14:24:01; Search time 26.53 Seconds (without alignments) 1806.242 Million cell updates/sec
 60.1
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Gapop 10.0 , Gapext 0.5
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1538
1 MCVGARRLGRGPCAALLLLG.....SFRTPIQEEQADAHSTLAKI 277
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                                                                                                                                                                                                                                                                                                                 sp_unclassified:*
sp_rvirus:*
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sp_archeap:*
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3 O9DDDZ

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          002764 oryctolagus
09ddd2 gallus gall
095407 homo sapien
016042 homo sapien
020041 mus musculu
099ne0 mus musculu
099rg7 xenopus lae
097ke0 rattus norv
062327 mus musculu
096j31 homo sapien
099ne1 mus musculu
099ne1 mus musculu
099ne2 mus musculu
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173 171 171 164.5 164.5 168.5 158.5 159.5 157.5 157.5 157.5 157.5 157.5 157.5 157.5 157.5 159.5 159.5 159.5 159.5 159.5 159.5	182.5 181.5 181.5 178 174
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3203 3203 461 651 186 655 655 655 655 655 655 655 655 655 6	430 203 430 387 401
1121124 111113 4 12211111	1444
09DYNE3 09DYNE3 091Y93 091Y93 091Y93 091Y98 092F87 09DFV0 09DFV0 09DFV1 091W77	Q969Z4 Q9BYU0 Q96JU1 Q96VD4 Q00300
Object mus musculu Object owpox viru Object mus musculu Object owpox viru	homo homo homo xen homo

## ALIGNMENTS

Query Match 60.1%; Score 924; DB 6; Length 267; Best Local Similarity 67.3%; Pred. No. 6.6e-77; Matches 177; Conservative 23; Mismatches 59; Indels 4; Gaps

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15 ALLLLGLGLSTVTGLHCVGDTYPSNDRCCHECRPGNGMVSRCSRSQNTVCRPCGPGFYND 74

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Tregaskes C.A.;
Thesis (2001), University of Reading, Re
EMBL; Au793700; CAC20218.1;
A LaterPro; IPR001005; Myb_DNA_bind.
R InterPro; IPR001368; TNFR_C6.
R Pfam; PF00020; TNFR_C6; 3.
R ProDom; PD000771; TNFR_C6; 1.
R PACOTTE; PS00037; MYB_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 3.
                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                          Query Match
Best Local
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Q1-MAR-2001 (TrEMBLrel. 1
Q1-MAR-2001 (TrEMBLrel. 1
Q1-DEC-2001 (TrEMBLrel. 1
HUMAN CD40-HOMOLOGUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9DDD2
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242
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hes 74; Conserv
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QPEE--
                       QPTEAWPRTSQGPSTRPVEVP-----GGRAVA
                                               TSDVICESSRRSSLSVLIPITAAVVTCLVGICIYCLVHTDLRRRGPKQAEAEAPRELVTQ
                                                                         SSDAICEDRDP---
                                                                                                                                                                                                              RLGRGPCAALLLLGLGLSTVTGLHCVGDTYPSNDRCCHECRPGNGMVSRCSRSQNTVCRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDSYKPGVDCAPCPPGHFS
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                                                                                                                                                CENGQYQHSWTKERHCTPHEICEDNAGLIVKRHGNATHNTVCQCRAGMHCSDASCQTCVE
                                                                                                                                                                       CGPGFY-NDVVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDS-----
                                                                                                                                                                                              RLGLLGLLCALLLGCG-QPGDAVNCSDKQYEHKGRCCNRCQPGKKLASECNDTEDSVCTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPRTAQGPSTPTLEASKGPQLAIVLSLGLGLGLLALLAALLALYLHQRAWR-PP---KLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVNYQACKPCTQCNRRSGSEPQQECTHTRDTVCRCRPGTQPLNGYKHGVDCAPCPQGHFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Metazoa;
                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                           14.98;
27.18;
VDFPVQETLLGGQPVA
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19,
                                                                                                                DCAPCPPGHFS--PGDNQACKPWTNCTLAGKHTLQPASN
                                                                                                                                                                                                                                               25;
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                           Score 229.5;
Pred. No. 2.
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261
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                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                       276;
                                                                      PARPITY
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ORESUL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O95407

O95407;

PRELIMINARY;

O1-MAY-1999 (TIEMBLIEL 10, Created)

O1-MAY-1999 (TIEMBLIEL 10, Last sequence update)

O1-DEC-2001 (TIEMBLIEL 19, Last annotation update)

DECOY RECEPTOR 3 (M68) (M68C) (M68E) (DJ583P15.1.1)

FACTOR RECEPTOR SUPERFAMILY, MEMBER 6B, DECOY).

DCR3 OR TR6 OR TNERSF6B.
                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                    SMARF: SMO208; TNFR: 3.

PROSITE; PS01186; EGF_2; UNKNOWN_1.

PROSITE; PS00652; TNFR_NGFR_1; UNKI

PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99253915; PubMed=10318773; Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.; Yu K.Y., Kwon B. S.; Yanon B. S.; Yu K.Y.; Ebner R., Ebner 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-99087326; Pubmed-9872321;
Pitti R.M., Marsters S.A., Lawren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-LUNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cluster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-PANCREAS;
MEDLINE-20122600; PubMed-10655513;
                                                                                                                                                                                              ProDom; PD000771; TNFR_c6; 1.
                                                                                                                                                                                                                                               Pfam; PF00020;
                                                                                                                                                                                                                                                                        InterPro; IPR000561; EGF-like.
InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (NOV-2001) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu Soderman A., Galloway S.M., Liu Q., Austin C.P., Cask Soderman A. Marker M.B./DR3 in human gastrointestinal "Overexpression of M68/DCR3 in human gastrointestinal independent of gene amplification and its location in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                       L; AF104419; AAD03056.1;
L; AF134240; AAD29688.1;
L; AF217796; AAF35244.1;
L; AF217793; AAF33685.1;
L; AF217794; AAF33686.1;
L; AL1211845; CAC03668.1;
L; BC017065; AAH17065.1;
P; O14763; 1D0G.
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                                                                                                                                                                                                                                            TNFR_c6;
   AA;
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   32679 MW;
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                                                                  UNKNOWN_1.
   F90AEE33718449AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNDIFFERENTIATED
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                                                                                                                                                                                                                             Receptor.
                                                                                                                                                                                                                                                      PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                Pfam; PF00020; TNFR_C6; 4.
ProDom; PD000771; TNFR_C6; 1.
SMART; SM00208; TNFR; 4.
PROSITE; PS00652; TNFR_NGER_1
                                                                                                                                                                                                                                                                                                                               intracellular, domain sequences.";
Cytokine 2:231-237(1990).
EMBL; S63368; AAB19824.2; -.
HSSP; P25942; ICDF.
                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                               Brockhaus M., Lesslauer W.;
                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91370690; PubMed=1966549; Dembic Z., Loetscher H., Gubler U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                    InterPro; IPR001368; TNFR_c6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 σ
                                                                                                                       CCHECRPGNGMVSRCSRSQNTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSER--KQLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSSEQCQPHRNCTALGLALNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --TQPLDSYKPG-------VDCAPCPPGHF--SPGDNQACKPWTNCTLAGKHTLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPTTCGPCPPRHYTQFWNY--LERCRYCNVLCGEREEEARACHATHNRACRCRTGFFAHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GW---
                                                 TREQURICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFS
                                                                          TATQDTVCRCRAG---
                                                                                                  CCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVP--ECLSCGSRCSSDQVETQAC
                                                                                                                                                                                                                                                                                                                                                                                  human TNF receptors have similar extracellular,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AWPRTSQGPSTRPVEVPGGRAVAAILGLGLVLGLLGPL--AILLALYLLRRDQRLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PASNSSDAICEDRDPPATQPQETQGPPARPI-----TVQPTE
NTTSSTDICRPHQICNVVA----IPGNASMDAVC----TSTSPTRSMAPGAVHLPQPVS
                      --PGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPATQPQETQGPPA----RPIT
                                                                                                                                                      66;
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                                                                                                                                                                                                                                                     TNFR_NGFR_1;
TNFR_NGFR_2;
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                                                                                                                                                   pred. No. 7.8
5; Mismatches
                                                                                                                                                               Score 216;
Pred. No. 7
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Pred. No. 6.5e-13;
                                                                          -TQPLDSYKPG-----
                                                                                                                                                                                                                 1B24A97E3AD4CF9F CRC64;
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                                                                                                                                                               DB 4;
.8e-12;
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                                                                                                                                                                         Length 425;
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                                                                 ----VDCAPCPPGHFS
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Q9Z0W1;
Q9Z0W1;
Q1-MAY-1999 (TrEMBLrel. 10,
Q1-MAY-1999 (TrEMBLrel. 10,
Q1-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                           Receptor
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50017; DEATH_DOMAIN; 1.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
PROSITE; PS00652; TNFR_NGFR_1; 3.
PROSITE; PS50050; TNFR_NGFR_2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00531; death; 1.
Pfam; PF00020; TNFR_C6; 4.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tuffereau C., Benejean J., Blondel D., Kieffer B., Flamand A.; "Low-affinity nerve-growth factor receptor (P75NTR) can serve as receptor for rables virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000488; Death.
InterPro; IPR000561; EGF-like.
InterPro; IPR000734; Lipase.
InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99077793; PubMed=9857182;
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                                                                                                                                                                                       DVVSATEPCKPCTECLGLQSMSAP---CVEADDAVCRCSYGYYQDEETGRCEACSVCGVG
                                                                                                                                                                                                                DVVS-SKPCKPCTWC-NLRSGSERKQLCTATQDTVCRCRAGTQPLDSY----
                                                                                                                                                                                                                                                                LLLLGLGLSTVTGLH-CVGDTYPSNDRCCHECRPGNGMVSRCSRSQNTVCRPCGPGF-YN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGI:97323; Ngfr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLII
                                    NLIPVYCSILAAVVVGLV
                                                            -- VPGGRAVAAILGLGLV 224
                                                                                                                                       SGLVFSCQDKQNTVCEECPEGTYSDEANHVDPCLPCTVCE-DTERQLRECTPWADAECEE
                                                                                                                                                                                                                                       LLLLLGVSFGGAKETCSTGMYTHSGECCKACNLGEGVAQPCGANQ-TVCEPCLDSVTFS
                                                                                     IPGRWITRSTPPEGSDVTTPSTQEPEAPPERDL-IASTVADTVTTVMGSSQPVVTRGTAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P07174; 1NGR
                                                                                                                                                                                                                                                                                        1 Similarity
78; Conserv
                                                                                                     ----RDPP----ATQP--QETQGPPARPITVQPTEAWPRTSQGPSTRPVE-----
                                                                                                                                                                                                                                                                                                                                                           417
                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                               KPGVDCAPCPPGHFSPGDNQA--CKPWTNCTLAGKHTLQPASNSSDAICED
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                                                                                                                                                                                                                                                                                                                                                           44686 MW;
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                                                                                                                                                                                                                                                                                                       13.8%;
                                    260
                                                                                                                                                                                                                                                                                           27;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                       Score 212.5; DB 1
Pred. No. 1.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                           5D7A4510DB8AF9B2 CRC64;
                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
                                                                                                                                                                                                                                                                                                                   DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                                                            98;
                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murinae;
                                                                                                                                                                                                                                                                                                                    417;
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                                                                                                                                       183
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RESULT

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Best Local S
Matches 59
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O99NEO;
O1-JUN-2001 (TREMBLIEL 17
? 01-JUN-2001 (TREMBLIEL 17
T 01-DEC-2001 (TREMBLIEL 1
TOAO TYPE V ISOFORM.
                                                                                                                                 091ZM6 PRELIMINARY;

091ZM6;

01-DEC-2001 (TrEMBLrel 19, 0

01-DEC-2001 (TrEMBLrel 19, 1

01-DEC-2001 (TrEMBLrel 19, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prodom; PD000771; TNFR_c6; 1.

SMART; SM00208; TNFR; 4.

PROSITE; PS00037; MYB 1; UNKNOWN_1.

PROSITE; PS00962; RIBOSOMAL_S2_1; UN

PROSITE; PS00652; TNFR_NGFR_1; 1.

PROSITE; PS50050; TNFR_NGFR_2; 4.

SEQUENCE 260 AA; 28895 MW; 57A5B
STRAIN-SPRAGUE-DAWLEY;
Osburg B., Peiser C., Doemling D., Schomburg L., Voigt K.,
"TNF-receptors p60 and p80 are constitutively expressed by
capillary endothelial cells and participate in TNF-alpha tr
                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) TUMOR NECROSIS FACTOR RECEPTOR TYPE II (FRAGMENT).
                                                                        Eukaryota; Metazoa;
Mammalla; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-21117110; PubMed-11172023;
Tone M., Tone Y., Fairchild P.J., W.
"Regulation of CD40 function by its
aiternative splicing.";
                                                   SEQUENCE FROM N.A
                                                                                                              Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                  187
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                                                                                                                                                                                                                                                                                                                                                                                                            VTGLH-----CVGDTYPSNDRCCHECRPGNGMVSRCSRSQNTVCRPCGPGFYNDVVSSK
                                                                                                                                                                                                                                                                      E-----DRD--PPATQ---PQETQGPP----ARPI
                                                                                                                                                                                                                                                                                                ATETTOTV - - - -
                                                                                                                                                                                                                                                                                                                                                                                            LTAVHLGQCVTCSDKQYLHDGQCCDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNRE
                                                                                                                                                                                                                                               EKVVKKPKDNEMLPPAARRQDPQEMEDYPGHNTAAPV
                                                                                                                                                                                                                                                                                                                      -TQPLDSYKPGVDCAPCPPGHFSPGDNQA-----CKPWTNCTLAGKHTLQPASNSSDAIC
                                                                                                                                                                                                                                                                                                                                             IRCHQHRHCEPNQGLRVKKEGTAESDTVCTCKEGQHCTSKDCEACAQHTPCIPGFGVMEM
                                                                                                                                                                                                                                                                                                                                                            - PCKPCTWCNLRSGSERKQLCTATQDTVCRCRAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pro; IPR001005; Myb_DNA_bind.
Pro; IPR001865; Ribosomal_S2.
Pro; IPR001368; TNFR_C6.
PF00020; TNFR_C6; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P25942; 1CDF
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                                                                                                           norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                               -CHPCPVGFFS----NQSSLFEKCYPWTSCEDKNLEVLQKGTSQTNVIC
                                                                                                             (Rat)
                                                                                     Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.8%;
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17,
                                                                                                                                                                                                                                                                                                                                                                                                                                          27;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 211.5;
Pred. No. 1.2e
27; Mismatches
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                                                                                                                                                            Created)
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Last annotation update)
                                                                                    Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.
57A5BACE8CF2F546 CRC64;
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ts isoforms
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No. 1.2
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                                                                                                 Vertebrata;
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ns generated
                                                                                      Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                          68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                     Euteleostomi;
; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   through
            Bickel
rat bra
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                                                                                      Rattus
             brain
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RESULT
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Best Local S
Matches 68
 Query Match
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01-MAY-2000 (TrEMBLrel. 13, Cr
01-MAY-2000 (TrEMBLrel. 13, La
01-JUN-2001 (TrEMBLrel. 17, La
01-JUN-2001 (TrEMBLrel. 17, La
                                                                  InterPro; IPR000488; Death.
InterPro; IPR000561; EGF-1ike.
InterPro; IPR000561; EGF-1ike.
InterPro; IPR001368; TNFR_c6.
Pfam; PF000531; death; 1.
Pfam; PF00020; TNFR_c6; 4.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 4.
PROSITE; PS00116; EGF_2; UNKNOWN
PROSITE; PS01166; EGF_2; UNKNOWN
PROSITE; PS010552; TNFR_NGFR_1; U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           through the blood-brain barrier.";
submitted (SEP-2001) to the EMBL/Ger
EMBL; AF420214; AAL16021.1; -.
Receptor.
NON_TER 1 1
NON_TER 433 433
SEQUENCE 433 AA; 45723 MW; 75736
                                  Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                             P75NTRA.
Xenopus laevis (African clawed frog).
Chordata; Craniata;
                                                                                                                                                                                     Submitted (JUL-1999) to the EMEMBL; AF172400; AAD51031.1; -. EMBL; AF172399; AAD51030.1; -. HSSP; P07174; 1NGR.
                                                                                                                                                                                                                                      neurotrophin receptor.";
                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                           Q9PRG7
                                                          PROSITE;
                                                                                                                                                                                                                                               Hutson L.D., Richards A
"Life and death in the
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                              NCBI_TaxID=8355
                                                                                                                                                                                                                                                                                                           Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LANCFILVQRKKKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPGHFS---PGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDP-PATQPQETQGPPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TKKQNRVCACNA-----DSYCALKLHSGNCRQCMKLSKCGPGFGVARSRTSNGNVICSAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATQDTVCRCRAGTQPLDSY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAKCPPGQYAKHFCNKTSDTVCADCAAGMFTQVWNH--LHTCLSCSSSCSDDQVETHNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                     PS50017; DEATH_DOMAIN; 1.
PS01186; EGF_2; UNKNOWN_1.
PS00652; TNFR_NGFR_1; UNKNOWN_3
PS50050; TNFR_NGFR_2; 3
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433
433
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433
45723 <sub>1</sub>
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                                   43419 MW;
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                                                                                                                                                                                                                                                           Bothwell
                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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Pred.
 Score
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                                   D13BCAF7863EFECF CRC64;
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No. 7.
 204
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13;
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Length
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                                                                                                                                                                       Matches
                                                                                                                                                                                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                         InterPro; IPR001368; TNFR_c6.

Pfam; PF00020; TNFR_c6; 3.

ProDom; PD000771; TNFR_C6; 1.

SMART; SM00208; TNFR; 3.

PROSITE; PS00652; TNFR_NGFR_1; 1

PROSITE; PS50050; TNFR_NGFR_2; 3

NON_TER 169 169

SEQUENCE 169 AA; 18525 MW; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CD40 PROTEIN (FRAGMENT).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9JKEO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-2001) to the EMBL; AF241231; AAF43717.2; HSSP; P25942; ICDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cytokine-inducible CD40 gene expression in vascular smooth muscle cells is mediated by nuclear factor kappaB and signal transducer are activator of transcription-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 62-169 FROM N.A.
STRALN-WISTAR, TISSUE-SMOOTH MUSCLE, AORTA;
MEDLINE-99330195; PubMed-10403401;
KIZESZ R., Wagner A.H., Cattaruzza M., Hecker M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-WISTAR; TISSUE-SMOOTH MUSCLE, AORTA; Gao D., Hecker M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Krzesz R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-WISTAR; TISSUE-SMOOTH MUSCLE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CWSGQYTAKGECCISCQVGEGVIKRCGVNQ-TVCEPCLDSVTYSDTISHTEACKPCTEC- 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CVGDTYPSNDRCCHECRPGNGMVSRCSRSQNTVCRPCGPGF-YNDVVS-SKPCKPCTWCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSDFPYTGTSVPPFDLSSSSA----TTSGDSKVLPPTGVAENLIPVYCSILAAVIAGLV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TQPQETQGPPARPITVQPTEAWPRTSQG-----PSTRPVE--VPGGRAVAAILGLGLV 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---CEKCPEGTYSDEDNDRDPCLPCTICE-DGEIEAKECTFTSDTVCYDPNPRVSSVTPA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --FGHKRMEAPCVESDDAVCACAYGYFTDKKSGQCKLCKSCPEGFGMMMSCTNIQDTI-- 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRSGSERKQL-CTATQDTVCRCRAG------
                         - PCKPCTWCNLRSGSERKQLCTATQDTVCRCRAG
                                                                      LTAVHLGQCVTCSDKQYLQGGECCDLCQPGNRLVSHCTALEKTQCQPCDSGEFSAHWNRE
                                                                                                                                                                         46;
                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hecker M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                       -CVGDTYPSNDRCCHECRPGNGMVSRCSRSQNTVCRPCGPGFYNDVVSSK 79
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                                                                                                                                                                                                13.2%;
29.1%;
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28; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ
                                                                                                                                                                    Score 203.5; DB 11
Pred. No. 4.1e-11;
9; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; E
Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                           F199D91EFA224A26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169
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                                                                                                                                                                                                                    DB 11;
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; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----TQPLDSYKP 121
                                                                                                                                                                                                                       169;
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Q62327;
01-NOV-1996
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VARIANT
SEQUENCE
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EMBL; X76401; CAA53981.1; -.
HSSP; P19438; INCF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD000771; TNFR_
SMART; SM00208; TNFR; 4
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                                                                                                                                                                                                                                                                                           ATQDTVCRCRAG-----
                                                                                                                                                                                                                                                                                                                                                                       CCHECRPGNGMVSRCSRSQNTVCRPCGPGFYNDVVSS-KPCKPCTWCNLRSGSERKQLCT 100
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  LALY - -
                                                                                             ARPITVQPTEAWPRTSQGPS:
                                                                                                                                                                                                                                                                                                                                           CCAKCPPGQYVKHFCNKTSDTVCADCEASMYTQVWNQFRTCLSCS-SSCSTDQVETRACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IRCHQHRHCELNQGLQVKKEGTAVSDTVCTCKEGQHCASKECETCAQHRPCGPGFGVVQM 134
                                                                                                                                                                                                                                           KQQNRVCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTFS
                                                                                                                                             DTTSSTDVCRPHRICSILA----IPGNASTDAVCAPESPTLSAIPRTLYVSQPEPTRS--
                                                                                                                                                                                        --PGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDP----PAT----QPQETQGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                             -QPLDQEPGPSQTPSILTSLGSTPIIEQSTKGGIS---
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48686
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  -LLRRDQRLP--PD
                                                                                             -----TRPV---EVPGGRAVAAILGLGLVLGLLGPLAIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                         34;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 201.5;
Pred. No. 1.8e
34; Mismatches
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-TQPLDSYKPG-----

---VDCAPCPPGHFS 134

97

Indels

79;

Gaps

14;

-LPIGLIVGVTSLGLLM

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"Amino acid variation in the tumor Necrosis linked to autoimmune diabetes in NOD mice."; Genomics 0:0-0(0).
                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95178848; PubMed-7873884; Powell E.E., Wicker L.S., Peterso "Allelic variation of the type 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MURINE TUMOUR NECROSIS FACTOR RECEPTOR
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                                                                                                                                                                                                 TNFR_NGFR_1;
TNFR_NGFR_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -CQPCPVGFFSNGSSLFEKCHPWTSC
                                                                                                                                                                                                                                                                                                                                                                  Peterson L.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
OR RECEPTOR 2 PROTEIN (F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                             K C H H S
                                                                          Y -> T.
F -> I.
S -> F.
Y -> C.
6C51D2CF1C4626DF CRC64;
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                                                                                                                                                                                                                                                                                                                                                  tumor necrosis factor receptor
201.5; Db ...,
No. 1.8e-10;
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                                                                                                                                                                                                                                                                                                                                                                  Todd J.A.;
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Best Local S
Matches 46
                                                                                                                                                                                   "Regulation or ....";
alternative splicing.";
alternative splicing.";
Artl. Acad. Sci. U.S.A. 9
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Q96J31;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY, MEMBER
(HERPESVIRUS ENTRY MEDIATOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q99NE1;
                                                                 InterPro; IPR001005; Myb_DNA_bind.
InterPro; IPR001865; Ribosomal_S2.
InterPro; IPR001368; TNER_c6.
Pfam; PF00020; TNER_c6; 4.
                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.
EMBL; AJ401389; CAC29429.1;
HSSP; P25942; 1CDF.
                                                                                                                                                                                                                                                       MEDLINE=21117110: PubMed=11172023; Tone M., Tone Y., Fairchild P.J., W. Regulation of CD40 function by its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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Submitted (PEB-2001) to the
EMBL; BC002794; AAH02794.1;
                        Prodom; PD000771; TNFR_c6; 1. SMART; SM00208; TNFR; 4.
                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD40 TYPE
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Mammalia; Eutheria;
  PROSITE;
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MYB_1; UNKNOWN_1
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Primates;
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Last annotation updat
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Pred. No. 4.7e
L4; Mismatches
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No. 4.7e-10;
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Matches 48
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f 01-JUN-2001 (TEMBLTel. 17
01-DEC-2001 (TEMBLTel. 1
01-DEC TII ISOFORM.
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Best Loc
Matches
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SMART; SM00208; TNFR; 4.

PROSITE; PS00037; MYB_1; UNKNOWN_1.

PROSITE; PS00962; RIBOSOMAL_S2_1; UNIPROSITE; PS00962; TNFR_NGFR_1; 1.

PROSITE; PS00652; TNFR_NGFR_2; 4.

SEQUENCE 234 AA; 25747 MW; 00DBI
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PROSITE;
PROSITE;
SEQUENCE
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MEDILINE-2117110; PubMed-11172023;

Tone M., Tone Y., Fairchild P.J., Wykes M., V

"Regulation of CD40 function by its isoforms
alternative splicing.";

Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(20)

EMBL; AJ401388; CAC29428.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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InterPro; IPR001865; Ribosomal_S2.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 4.
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135
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                                                                                                                                                                                                                                 VTGLH-----CVGDTYPSNDRCCHECRPGNGMVSRCSRSQNTVCRPCGPGFYNDVVSSK
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ATETTDTV-
                                        -TQPLDSYKPGVDCAPCPPGHFSPGDNQA-----CKPWTNCTLAGKHTLQPASNSSDAIC
                                                                                        IRCHQHRHCEPNQGLRVKKEGTAESDTVCTCKEGQHCTSKDCEACAQHTPCIPGFGVMEM
                                                                                                                                      -PCKPCTWCNLRSGSERKQLCTATQDTVCRCRAG-----
                                                                                                                                                                                   LTAVHLGQCVTCSDKQYLHDGQCCDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNRE
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PS00652; TNFR_NGFR_1; 1.
PS50050; TNFR_NGFR_2; 4.
222 AA; 24499 MW; EE:
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                                                                                                                                                                                                                                                                            Score 193.5;
Pred. No. 4.8e
23; Mismatches
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Last annotation update)
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EE21E6C76FB42DEF CRC64;
NQSSLFEKCYPWTSCEDKNLEVLQKGTSQTNVIC
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No. 4.5e-10;
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186
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Best Local S
Matches 78
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Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Macaca.

MCBI_TaxID=9541;
TISSUE=KIDNEY;
MEDLINE=99296730; PubMed=10366573;
Foster T.P., Chouljenko V.N., Kousoulas K.G.;
"Functional characterization of the HveA homo
                                                                                                                                                                                                                                                               Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9XSZ8;
01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai

Suzuki Y., Sugano S., Hashimoto K.;

"Isolation of full-length cDNA clones from macaque brain
libraries.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8ZSX6D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001368; TNFR_c6.
SMART; SM00208; TNFR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases EMBL; AB046039; BAB01621.1; -.
                                                                                                                                                                                                                                   Cercopithecinae;
NCBI_TaxID=9534;
                                                                                                                                                                                                                                                                                                                                                                                                                                HVEAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HVEAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 LLLLGLGLSTVTGLHCVGDTYPSNDRCCHECRPGNGMVSRCSRSQNTVCRPCGPGFYNDV 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HKEVGPGPGGGGSGINPAYRT--EDVNEDTIGVLVRL 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HK------PPGGGS-----FRTPIQEEQADAHSTLAKI 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AWPRTSQGPSTR----PVEVPGGRAVAAILGLGLVLGLLGPLAILLALYLLRRDQRLPPDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APLGIHGCDEWGRRARRGVEVAAGASSGGE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LMLLPWPLATLT-----STTLWQCPPGE--EPDLNPGQGTLCRPCPPGTFSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPATQPQETQGPPARPITVQPTE 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSSKPCKPCTWCNLRSGSERKQLCTATQDTVC-RCRAGTQPLDSYKP-GVDCAPCPPGHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -GNGTRAGGPEETAAQYAVIAIVPVFCLMGLLG----ILVCNLLKR-KGYHCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.5%;
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Pred. No. 1.4e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BA8DE92593E1E859 CRC64;
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       HveA homolog specified by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Best Local :
                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                    green monkey kidney cells with a green fluorescence protein."; Virology 258:365-374(1999).
EMBL; AF147720; AAD37381.1; -.
HSSP; O14763; 1D0G.
                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00652; TNFR_NGFR_1; PROSITE; PS50050; TNFR_NGFR_2; SEQUENCE 283 AA; 30199 MW;
                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00020; TNFR_C6; 3. ProDom; PD000771; TNFR_C6; 1. SMART; SM00208; TNFR; 3.
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                                                    170
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                                                                                                                                                                                                                                          12 PCAALLLIGIGISTVTGLHCVG------DTYPSNDRCCHECRPGNGMVSRCSRSQNTV 63
                                                                                                                                                                                     CRPCGPGFY----NDVVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDSY 119
                                                                                                                        KPGVDCAPCPPGHF---SPGDN-QACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPATQ
                                                                                                                                                           CEPCSPGTYIAHFNGL---SKCLQCQMCDPAMGLRTSRNCSTTANALC---
                                                                                                                                                                                                                 PKADILTLVLYL-TFLGSSCYAPALPSCKEDEYPVGSECCPKCGPGFHVRQACGEQTGTV
LIICVKRRKSR 234
                         LALYLLRRDQR 245
                                                                             PQETQGPPARPITVQPTEAWPRTSQGPSTRPVEVPGGRAVAAIL-GLGLVLGLLGPLAIL
                                                  -FSSNGTLEECQHGNKCSKWLVTEAGPGT
                                                                                                        -----GCSPGHFCIIQDGDHCAACRAYATSS-PGQRVQKGGTESQDTLCQN-CPPGT-
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                                                                                                                                                                                                                                                                                     Similarity
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26.3%;
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                                                                                                                                                                                                                                                                     Score 190.5; 1
Pred. No. 1.1e
29; Mismatches
                                                                                                                                                                                                                                                                                                                                        397951C6617FE3AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                   UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           herpes simplex virus expressing
                                                                                                                                                                                                                                                                                     No. 1.1e-09
                                                    -SSSRWVWWLLSGSLIVIVIVGLIILR
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12;

Search completed: June 18, 2002, Job time: 135 sec 14:26:16

African

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Result
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Perfect score:
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being part and is derived by analysis of the total score distribution.
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1: /SIDS1/gcgdata/h
2: /SIDS1/gcgdata/h
3: /SIDS1/gcgdata/h
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| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*
| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*
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Listing first 45 summaries
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1538
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Copyright (c) 1993 - 2000 Comp
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AAR79904
AAB35329
AAB50522
AAR76996
AAR81882
AAW48976
AAB66985
AAR81881
AAW48977
                                                                                                                                                                                                                                                                                         SUMMARIES
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ACT-4 cell surface ACT-4 h-1 receptor Human 0x40 protein Human tumour necro Deduced sequence e Plasmid pDC406/0x4 0X40/Fc mutein. C 0x40 protein. Uni Mouse type-II memb Mouse type-II memb Mouse ox40 extracellula
                                                                                                                                                                                                                                Description
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## ALIGNMENTS

Cell surface receptor; ACT-4; T-lymphocyte; T-cell; immune system. ACT-4 cell surface receptor protein. AAR74737; 03-NOV-1994; Domain Cleavage-site Cleavage-site Homo 21-NOV-1995 (first entry) AAR74737 standard; Protein; 277 11-MAY-1995. WO9512673-A. Modified-site Modified-site Peptide sapiens. 94WO-GB02415 /note= "0 /note= "s 146..148 /note= "g 214..240 /note= "signal peptide" 22..23 24..25 Location/Qualifiers /note= "signal cleavage site" "glycosylation site" "signal cleavage site" "transmembrane domain" "glycosylation site" A

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RESULT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence encodes the full-length cell surface receptor ACT-4 isolated from activated CD4+ T-lymphocytes. The sequence may be expressed in e.g. COS-7 cells. The encoded protein, its ilgands or fragments, and antibodies may be used for the treatment of transplant rejection, graft-versus-host disease, autoimmune disease, etc.
                                                                                                                                                               Homo
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useful
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GPPARPITVQPTEAWPRTSQGPSTRPVEVPGGRAVAAILGLGLVLGLLGPLAILLALYLL
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                            RRDQRLPPDAHKPPGGGSFRTPIQEEQADAHSTLAKI
                                                gpparpitvqpteawprtsqgpstrpvevpggravaailglglvlgllgplaillalyll
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llarity 100.0%;
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18-AUG-1999;
20-AUG-1999;
10-SEP-1999;
                                                                                                                                                                                                                                                                                                                              The present invention provides the protein and coding sequences of the human tumour necrosis factor receptors TR13 and TR14. These sequences useful in the diagnosis and treatment of many diseases, including cancautoimmune diseases, cardiovascular disorders, allergies,
                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding 2 human tumor necrosis factor receptor polypeptides ((TR13)) and (TR14)), useful for the prevention, diagnosis and treatment of, e.g. cancers, acquired immune deficiency syndrome and hypohidrotic ectodermal dysplasia.
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                                                                                                                                                                                                                                                                                   Sequence
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rrdqrlppdahkppgggsfrtpiqeeqadahstlaki
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277; Conserv
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                                                                                                                                                                                                                                                                                                                    graft rejection, inflammation, aneurysms and
                                                                                                                                                                                                                                      Score 1538;
Pred. No. 1
                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                     1.2e-100;
  277
                                                                                                                                                                                                                                                  DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disease;
                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infection;
                                                                                                                                                                                                                                                  277;
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                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                               of the
                                                                                                              180
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                                                                                                                                                                                                                                                                                                                                          cancer,
                                                                                                                                                                                                                                                                                                                                                     are
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RESULT
AAB50522
ID AAB5

AAB50522

standard;

Protein;

277

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61

NTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDSYK

Query Match Best Local S Matches 277

Similarity

100.0%;

Conservative

0;

Score 1538; Pred. No. 1.2 ); Mismatches

DB 22; ..2e-100; s 0;

Indels Length

0

Gaps

0

60 60 277;

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CC factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without CC intracellular domain, also referred to as tumour necrosis factor CC receptor 5 (TNF) solvents, and referred to as tumour necrosis factor CC receptor 5 (TNFR)-5 or TRS)). TRID has cytostatic, immunosuppressive, CC nootropic, neuroprotective, antiviral, antiinflammatory, anticonvulsant, CC antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic activities, and can be used in gene therapy. The TRID polynucleotides CC are useful for detecting complementary polynucleotides. TRID proteins and CC polynucleotides are useful in the treatment of tumours, resistance to CC parasite, bacteria and viruses, restenosis and graft versus host disease. CC They are also useful for inducing proliferation of T-cells, endotheilal CC ells and certain haematopoletic cells, to regulate antiviral responses CC and to prevent certain autoimmune diseases after stimulation of TRID by CC an agonist or TRAIL binding facilitator. The antibodies which bind TRID CC associated with increased or decreased apoptotic cell death. The TRID CC useful in the diagnosis, treatment or prevention of: (a) cancer; CC useful in the diagnosis, treatment or prevention of: (a) cancer; CC is autoimmune discases associated with increased CC apoptosis; (d) cardiovascular disorders; and (e) viral infection. The presents a tumour necrosis factor receptor used in CC comparison with TRID in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRAIL receptor without intracellular domain; diagnosis; cytostatic; tumour necrosis factor related apoptosis inducing ligand; vasotropic; inmunosuppressive; neuroprotective; antiviral; antiinflammatory; antiparasitic; cardiant; anti-HIV; antiparkinsonian; gene therapy; restenosis; graft versus host disease; tumour; cancer; apoptotic cell death related disease; autoimmune disorder; cardiovascular disorder; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid encoding a TRID polypeptide, also referred to as necrosis factor receptor 5, useful in the diagnosis, treatment prevention of cancer, autoimmune disorders and viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; tumour necrosis factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-NOV-2000
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens.
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277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as tumor
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RESULT
AAR76996
ID AAR7
C the OX-40 antigen was identified (expressed on the surface of activated autoantigen-specific CD4+ T-cells present at the site of inflammation but absent on CD4+ T-cells at non-inflammatory sites) C and cDNA encoding the antigen was isolated. PCR primers were designed and used to clone murine OX-40 cDNA by PCR from RNA C isolated from murine CD4+ T-cells activated with concanavalin A. C Then the murine OX-40 cDNA was used to probe a cDNA lambda gtl1 C library from human activated T lymphocytes to obtain human OX-40 cDNA. The published patent application states that the OX-40 cDNA c sequence is also in SQ ID no. 1, but this sequence is not present in the spec. A nucleic acid having the sequence in SQ ID no 1 and C the polypeptide encoded by it are claimed.
                                                                                                                                                                                                                                                                antigen activated \tilde{T}-cells, especially, for example, CD4+ T-cells. A human CDNA encoding the human OX-40 homologue was cloned as follows. Using the Experimental Autolumnune Encephalomyelitis model in rats the OX-40 antigen was identified (expressed on the surface of
                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Fig 11; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                             Antigen OX-40 is specifically expressed on the cell surface of
                                                                                                                                                                                                                                                                                                                                                                                                                                                        activated T-cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid encoding an activated T-cell antigen, Ox-40 - used develop prods. for detection and therapy of conditions mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1995-283771/37.
N-PSDB; AAQ93257.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-FEB-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Ox-40; activated T-cells; CD4+ T-cells; antigen;
multiple sclerosis; sarcoldosis; rheumatoid arthritis; uveitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deduced
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(CANT-) CANTAB PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-AUG-1995
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Sequence

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RESULT
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Best Local (
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                              used to transform the CV-1/EBNA (ATCC CRL 10478) monkey kidney cel
line. Culture supernatant was purified by affinity chromatography
and this was used, together with labeled goat anti-human IgG to
                                                                                                                                                     New isolated DNA encoding the OX40 ligand polypeptide and host cells, used to produce recombinant ligand used prim. T cell culture, to modulate immune response etc.
                                                                  and is used to express a soluble OX40/Fc mutein fusion pruse in detecting cDNA clones encoding a OX40 ligand. The fragment may be derived from human IgG1, and the plasmid
                                                                                                                                                                                                     WPI; 1995-357992/46.
N-PSDB; AAT00829.
                                                                                                                                                                                                                                                                                                                                                                                                                    OX40; OX40-L;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid pDC406/OX40/Fc* encoding an OX40/Fc mutein protein.
                                                                                                                                                                                                                                       Baum
                                                                                                                                                                                                                                                                                     23-JUL-1993;
                                                                                                                                                                                                                                                                                                           23-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                           US5457035-A
                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                       pDC406/0X40/Fc*;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR81882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR81882 standard;
                                                                                                                               Example
                                                                                                                                                                                                                                                            (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                   10-OCT-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                       PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NTYCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDSYK 120
                                                                                                      plasmid encodes an OX40/Fc antibody fragment mutein protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RRDQRLPPDAHKPPGGGSFRTPIQEEQADAHSTLAK 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPPARPITVQPTEAWPRTSQGPSTRPVEVPGGRAVAAILGLGLVLGLLGPLAILLALYLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                269;
                     various
                                                                                                                              2; Column 35-38; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                       Fanslow WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
                                                                                                                                                                                                                                                                                                                                                                                                                  cytokine; cell surface molecule; plasmid;
                     cell
                                                                                                                                                                                                                                                                                    93US-0097827
                                                                                                                                                                                                                                                                                                           93US-0097827
                                                                                                                                                                                                                                                                                                                                                                                                      membrane glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
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97.5%;
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                                                                                                                                                                                                                                       RB,
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Pred. No. 1
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                                                                                                                                                                                                                                       Goodwin RG;
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L.1e-97;
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                                                                                 The Fc
                                                                                           protein for
                                                                                                                                                                  also vectors in e.g.
                                                                      may be
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DB 16;

Length

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RESULT
ARAW48976
ID AAW4 8976
ID AAW4 8976
ID AAW4 876
ID CAAW4
XX AAW4 876
ID CAAW4
XX OX4C
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Best Local
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Chimeric
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OX40/Fc mutein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OX40/Fc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW48976 standard;
                     Example
                                                    Purified polypeptide OX-40 ligands - production and binding assays for OX-
                                                                                                                                                                   Baum
                                                                                                                                                                                                    (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                         23-JUL-1993;
22-JUN-1995;
                                                                                                                                                                                                                                                                                               22-JUN-1995;
                                                                                                                                                                                                                                                                                                                                     21-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                        US5783665-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPL--DSYKPGVDCAPCPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ttvwprtselpstptlvep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hfspgnngackpwtnctlsgkgtrhpasdsldavcedrsllatllwetgrptfrpttvgs
                                                                                                                                                                 PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TEAWPRISQGPSTRPVEVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HFSPGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPATQPQETQGPPARPITVQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        eavnydtckqctqcnhrsgselkqnctptqdtvcrcrpgtqprqdsgyklgvdcvpcppg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 all11g1t1gvtarr1ncvkhtypsghkccrecqpghgmvnrcdhtrdt1chpcetgfyn
                                                                                                                             1998-427099/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126;
                     2
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                                                                                                             AAV32636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytokine;
                                                                                                                                                                 Fanslow WC,
                     Col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus
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                     37-40;
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95US-0494574
                                                                                                                                                                                                                                                                                                 95US-0494574
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225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Extracellular domain of mouse OX40"
207..438
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                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T cell antigen; TH-2 immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein; 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.0%;
                   26pp; English
                                                                                                                                                                                                                                                                                                                                                                                                           "changed mutant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "changed
mutant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "changed
mutant"
                                                                                                                                                                 Gayle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Mutant Fc region of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 676.5; DB Pred. No. 7e-40;
                                                                                                                                                                 RB,
                                                                                                                                                                                                                                                                                                                                                                                                                            from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from
                                                       ; - for co:stimulation of T-cell
OX-40 and homologues
                                                                                                                                                                 Goodwin
                                                                                                                                                                                                                                                                                                                                                                                                                          Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leu in wild-type to Ala
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                                                                                                                                                                 RG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                            wild-type
                                                     homologues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OX40-L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189
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밁 δÃ 밁 δÃ

190 192 130 132

ttvwprtselpstptlvep

208

TEAMPRISOGPSTRPVEVP 210

HFSPGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPATQPQETQGPPARPITVQP

191

189

hfspgnngackpwtnctlsgkgtrhpasdsldavcedrsllatllwetgrptfrpttvqs

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В
                               Qy
                                                                    B
                                                                                                 Q
                                                                                                                                      Matches
                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                  The present sequence represents the OX40/Fc fusion protein that contains the extracellular domain of mouse OX40 fused to the mutated Fc region of the human IgGl antibody. The fusion protein was used for detecting cDNA clones encoding an OX40 ligand. The invention claims for a murine OX40-L cytokine (AAW48975) that binds to the murine T cell antigen, OX40. The OX40-L protein is claimed to be useful for co-stimulation of T-cell production and in binding assays for detecting OX40 or its homologues. The OX40-L protein is also claimed to generate a TH-2 immune response.
                                                                                                                                                                                                                      Sequence
   70
                                  74
                                                                    10
                                                                                                     15
                 allllgltlgvtarrlncvkhtypsghkccrecqpghgmvnrcdhtrdtlchpcetgfyn
                                                                                     ALLLLGLGLS-TVTGLHCVGDTYPSNDRCCHECRPGNGMVSRCSRSQNTVCRPCGPGFYN 73
eavnydtckqctqcnhrsgselkqnctptqdtvcrcrpgtqprqdsgyklgvdcvpcppg
                                                                                                                                      126;
                                                                                                                                    Similarity 63.3
26; Conservative
                                                                                                                                                                                                                        438 AA;
                                                                                                                                                      44.0%;
63.3%;
                                                                                                                                      17;
                                                                                                                                    Score 676.5; DE
Pred. No. 7e-40;
7; Mismatches
                                                                                                                                                                     DB 19;
                                                                                                                                      53;
                                                                                                                                    Indels
                                                                                                                                                                  Length
                                                                                                                                    Ψ
                                                                                                                                    Gaps
                                                                    69
                                  131
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2

## RESULT AAB66985 Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia; multiple sclerosis; osteoprorosis; osteomyelitis; asthma; inflammation; systemic lupus erythematosus; graff-versus-host disease; septic shock; acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pacoronary condition; myocardial infarction; cancer; diabetes; psoriasis 0x40 Unidentified endometriosis; fever; glomerulonephritis; inflammatory ischaemia; Parkinson's disease. 09-JUL-1999; 09-DEC-1999; 07-JUL-2000; WO200103719-A2 19-APR-2001 AAB66985; AAB66985 (AMGE-) AMGEN 18-JAN-2001. 8 protein. standard; 2000WO-US18667 (first entry) 99US-0350670 99US-0457647 Protein; 205 B

psoriasis;
disease;

pain;

Treating conditions leading to bone loss such as rheumatoid arthritis, multiple sclerosis and asthma, comprises administering an

O

ė

inhibitors

WPI; 2001-103031/11

Boyle WJ,

Lacey DL,

Calzone

Ľ,

Chang ĭ

Senaldi

စ

osteoprotegerin protein in conjunction with interleukin and tumor necrosis factor alpha

<u>ب</u>

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RESULT
AAR01881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a method for treating conditions leading CC to bone loss. The method comprises administering a purified and isolated osteoprotegerin (OPG) protein (AAF57836-AAF57838 and AAB66974-AAB66976) CC in conjunction with other substances such as tumour necrosis factor-alpha CC (TNF-alpha) inhibitors, interleukin (II)-6, -8 and -18 inhibitors, ICE CC modulators, fibroblast growth factor (FGF)1-10 modulators and/or platelet CC activating factor (PAF) antagonists. The method is useful for treating CC conditions leading to bone loss such as rheumatoid arthritis, multiple CC sclerosis, osteoporosis, osteopyelitis and asthma. The method is also CC useful for treating inflammation, systemic lupus crythematosus (SLE) and Graft-versus-host disease (GvHD). Other diseases that can be treated CC include acute pancreatitis, Alzheimer's disease, anorexia, CC annear, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia, CC inflammatory bowel disease, ischaemia, pain, Parkinson's disease, concared concared to the present sequence was used in a sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                        WPI; 1995-357992/46
                                                                                                                                                                                                                                                               membrane
                                                                                                                                                                                                                                                                                                                                                                       AAR81881;
                                                    Baum PR,
                                                                                                                 23-JUL-1993;
                                                                                                                                              23-JUL-1993;
                                                                                                                                                                            10-OCT-1995
                                                                                                                                                                                                        US5457035-A
                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                OX40; OX40-L;
                                                                                                                                                                                                                                                                                                           Mouse type-II membrane polypeptide OX40 extracellular domain.
                                                                                                                                                                                                                                                                                                                                        08-JUL-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                  AAR81881 standard; Protein; 206 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190
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tvwprtsqlpst 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EAWPRTSQGPST 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FSPGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPATQPQETQGPPARPITVQPT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             avnydtckqctqcnhrsgselkqnctptedtvcqcrpgtqprqdsshklgvdcvpcppgh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPL--DSYKPGVDCAPCPPGH 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       afll1gls1gvtvklncvkdtypsghkccrecqpghgmvsrcdhtrdtvchpcepgfyne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fspgsnqackpwtnctlsgkqirhpasnsldtvcedrsllatllwetqrttfrpttvpst 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                               glycoprotein.
                                                      Fanslow WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                             cytokine;
                                                                                                                 93US-0097827
                                                                                                                                              93US-0097827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         316pp; English.
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                                                      Gayle
                                                                                                                                                                                                                                                                               cell surface molecule.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 676;
Pred. No. 3
                                                      RВ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                      Goodwin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22;
.5e-40;
                                                      RG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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RESULT 10
AAW48977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SX CCC X PX PT PX X R
                                                                                                                                                                                                                                                                                                                                                                                                                            밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 43.9
Best Local Similarity 64.8
Matches 125; Conservative
                    Example 1; Col 33-34;
                                       Purified polypeptide OX-40 ligands - for production and binding assays for OX-40 a
                                                                                   WPI; 1998-427099/36.
                                                                                                                                                                                                                                                                                                                                                                     AAW48977 standard; Protein; 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated DNA encoding the OX40 ligand polypeptide - also ve and host cells, used to produce recombinant ligand used in e.g. prim. T cell culture, to modulate immune response etc.
                                                                          N-PSDB;
                                                                                                         Baum
                                                                                                                             (IMMV ) IMMUNEX CORP
                                                                                                                                                   23-JUL-1993;
22-JUN-1995;
                                                                                                                                                                                    22-JUN-1995;
                                                                                                                                                                                                        21-JUL-1998
                                                                                                                                                                                                                              US5783665-A
                                                                                                                                                                                                                                                  Mus sp.
                                                                                                                                                                                                                                                                        OX40/Fc
                                                                                                                                                                                                                                                                                  OX40; cytokine; T cell antigen; TH-2 immune response; OX40-L;
                                                                                                                                                                                                                                                                                                        Mouse 0X40 extracellular domain
                                                                                                                                                                                                                                                                                                                             25-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence encodes the extracellular domain of OX40, a membrane {
m glycoprotein} present on the CD4 positive subset of activated T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAT00826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Column 33-34; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130
                                                                                                                                                                                                                                                                                                                                                                                                                                                 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132
                                                                                                                                                                                                                                                                                                                                                                                                                           190 ttvwprtselpst 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 ALLLLGLGLS-TYTGLHCVGDTYPSNDRCCHECRPGNGMVSRCSRSQNTVCRPCGPGFYN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                      TEAWPRTSQGPST 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HFSPGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPATQPQETQGPPARPITVQP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eavnydtckqctqcnhrsgselkqnctptqdtvcrcrpgtqprqdsgyklgvdcvpcppg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        allllgltlgvtarrlncvkhtypsghkccrecqpghgmvnrcdhtrdtlchpcetgfyn
                                                                          AAV32640.
                                                                                                         Fanslow WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206
                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                   93US-0097827.
95US-0494574.
                                                                                                                                                                                    95US-0494574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.98;
                   26pp; English.
                                                                                                         Gayle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 675.5;
Pred. No. 3.0
                                                                                                         RВ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                         Goodwin
                                        c co:stimulation and homologues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .8e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                    of T-cell
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The present sequence represents the mouse OX40 extracellular domain

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RESULT 1
AAW94649
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Best L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The extracellular domain of OX40 is its ligand binding domain. The cDNA (AAV32640) encoding OX40 extracellular domain was used in the construction of the chimeric OX40/Fc cDNA (AAV32640). The invention claims for a murine OX40-L cytokine (AAM48975) that binds to the OX40 murine T cell antigen. The OX40-L protein is claimed to be useful for co-stimulation of T-cell production and in binding assays for detecting OX40 or its homologues. The OX40-L protein is also claimed
                                                                                                                                                                                                                                                                                                                                             Tumour necrosis factor receptor; TNF-R; autoimmune diseases; inflammation; septic shock; cachexia; graft versus host diseskin allergic reaction; immune complex disease; malaria;
                                                               New compounds designed from a binding loop of a tumour necrosis factor receptor - are capable of inhibiting the biological activities of tumour necrosis factor, e.g., in treating inflammor autoimmune diseases
                                                                                                                               WPI;
                                       Disclosure;
                                                                                                                                                                                                                                                         03-DEC-1998
                                                                                                                                                                                                                                                                                  W09853842-A1
                                                                                                                                                                                                                                                                                                                                                                                                 TNF-R extracellular Cys-rich domain OX40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW94649 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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             The present
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                                                                                                                                                                                                                                29-MAY-1998;
                                                                                                                                                                                                                                                                                                          Homo
                                                                                                                                                                                                                                                                                                                                    transplantation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW94649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DVVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPL--DSYKPGVDCAPCPPG 131
                                                                                                                                                                                                                                                                                                         sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALLLLGLGLS-TVTGLHCVGDTYPSNDRCCHECRPGNGMVSRCSRSQNTVCRPCGPGFYN 73
                                                                                                                               1999-080781/07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hfspgnngackpwtnctlsgkgtrhpasdsldavcedrsllatllwetgrptfrpttvqs 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HFSPGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPATQPQETQGPPARPITVQP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eavnydtckqctqcnhrsgselkqnctptqdtvcrcrpgtqprqdsgyklgvdcvpcppg
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                                                                                                                                                       MI,
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                                                                                                                                                      Murali R,
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              invention
                                     Fig 1; 78pp;
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                                                                                                                                                                                PENNSYLVANIA.
                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                        97US-0866545
                                                                                                                                                                                                                                98WO-US10891
                                                                                                                                                                                                                                                                                                                                    rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43.9%;
 sequence to
              describes
                                                                                                                                                       Takasaki
                                                                                                                                                                                                                                                                                                                                              ock; cachexia; graft versus host disease;
immune complex disease; malaria;
                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 675.5; DB 1
Pred. No. 3.8e-40;
6; Mismatches 49
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peptides and peptide analogues to a binding loop of a tumour ne
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                                                                             inflammation
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              which
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a tumour necrosis

osteoclastogenesis and bone resorption. Osteoclastogenesis and bone resorption inhibiting peptide analogues from the present invention have osteopathic, cytostatic, antirheumatic, antiarthritic, antiinflammatory and immunomodulatory activities, and are tumour necrosis factor (TNF).

The present invention describes a method for inhibiting

Fig

1:

81pp; English.

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Best Local S
Matches 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                factor receptor (TNF-R) superfamily member. The compounds are est designed from a binding loop of TNF-R p55. They are capable of inhibiting TNF binding to its cellular receptors and may be used inhibit the biological activities of TNF. They may be used in triple the property of the pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             osteoclastogenesis; bone loss; bone resorption; osteopathic; cytost. antirheumatic; antiarthritic; antiinflammatory; immunomodulatory; tumour necrosis factor related activation induced cytokine; TRANCE; receptor activator of NF-kappaB ligand; RANK; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYPE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Paget's disease; metastatic bone disease; rheumatoid arthr periodontal disease; modulating dendritic cell maturation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumour necrosis factor receptor; TNF-R; inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human TNF-R extracellular Cys-rich domain OX40 SEQ ID NO:10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                     (BARO/)
                                                                                                                                                                                                                                                                                                                                                                                                             (HORN/)
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                                                                                                                                                                                                of peptides and peptide analogs which are \texttt{TRANCE/RANK} inhibitors, inhibiting osteoclastogenesis and bone resorption -
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                                                                                                                                                                                                                                                                                  2001-182866/18.
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56; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             UNIV PENNSYLVANIA
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                                                                                                                                                                                                                                                                                                                                  Horne WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 AA;
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llarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                     R. C.
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                                                                                                                                                                                                                                                                                                                                     Baron
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                                                                                                                                                                                                                                                                                                                                  Greene MI,
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2.2e-16;
                                                                                                                                                                                                                                                                                                                                     Murali
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          osteopathic; cytostatic;
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Best Local S
Matches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes the human TRID protein (tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without intracellular domain, also referred to as tumour necrosis factor receptor 5 (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive, nootropic, neuroprotective, antiviral, antiinflammatory, anticonvulsant, antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic activities, and can be used in gene therapy. The TRID polynucleotides are useful for detecting complementary polynucleotides. TRID proteins an polynucleotides are useful in the treatment of tumours, resistance to parasite, bacteria and viruses, restenosis and graft versus host disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TRS; nootropic TRAIL receptor without intracellular domain; diagnosis; cytostatic; tumour necrosis factor related apoptosis inducing ligand; vasotropic; immunosuppressive; neuroprotective; antiviral; antiinflammatory; anticonvulsant; antiparasitic; cardiant; anti-HTV; antiparkinsonian; gene therapy; restenosis; graft versus host disease; tumour; cancer; apoptotic cell death related disease; autoimmune disorder;
                                                                                                                                                                                                            Nucleic acid encoding a TRID polypeptide, also referred to as tumor necrosis factor receptor 5, useful in the diagnosis, treatment or prevention of cancer, autoimmune disorders and viral infection - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NF-kappaB ligand (RANK) inhibitors. The method is useful for treating diseases characterised by bone loss such as osteoporosis, Paget's disease, metastatic bone disease, rheumatoid arthritis or periodontal
                                                                                                                                                                                 Disclosure; Fig 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB36700 standard; Protein; 415
                                                                                                                                                                                                                                                                                                                                                                             20-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 apoptotic cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human tumour necrosis factor receptor LTbR protein SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN
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                                                                                                                                                                                                                                                                                                              Ruben
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                                                                                                                                                                                                                                                                                                                                                                                                           2000WO-US13515
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                                                                                                                                                                                                                                                                                                              SM,
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                                                                                                                                                                                                                                                                                                                                                                             99US-0135164
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                                                                                                                                                                               285pp;
                                                                                                                                                                                                                                                                                                              Gentz RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
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                                                                                                                                                                                 English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytokine (TRANCE)/ receptor activator of hibitors. The method is useful for treating
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Pred. No. 1.4e-15;
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Best Local :
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                                                                                                                                                                                                                           RANK
14-OCT-1997;
23-DEC-1996;
                                                                                                                                                                                                                                                                                   AAW69951;
                                                                                                                                                                                                                                                                                                                 AAW69951 standard;
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                                          22-DEC-1997;
                                                                       02-JUL-1998
                                                                                                     W09828426-A2
                                                                                                                                                                             RANK; necrosis factor-kappa B; NF-kB; receptor activator;
immune response; inflammatory response; toxic shock; seps:
                                                                                                                                                                                                                                                       08-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                            360
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                                                                                                                                                                                                                                                                                                                                                                                         vlggtrgpgdppappeppyptpeegapgpselstpyqed
                                                                                                                                                                                                                          polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aecrcqpgmscvyldnecvhceeerlvlcqpgteaevtdeimdtdvncvpckpghfqnts 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVCRCRAG-----TQPLDSYKPG------VDCAPCPPGHF--SP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRPGNGMVSRCSRSQNTVCRPCGPGFYNDVVSS-KPCKPCTWCNLRSGSERKQLCTATQD 104
                                                                                                                                                                                                                                                                                                                                                                                                                        -----RDQRLPPDAHKP-----PGGGSFRTPIQEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    tapsleevvlqqqsplvqareleaepgehgqvahgangihvtg--gsvtvtgn1y1yngp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cawmrhpslcrklgtllkrhpegeesppcpapradphfpdlaepllpmsgdlspspagpp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPAT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cppgefvfavcsrsqdtvcktcphnsynehwnhlstcqlcrpcdivlgfeevapctsdrk 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rlprasspcglawgplllglsgllvasqpqlvppyr1enqtcwdqdkeyyepmhdvccsr 61
                                                                                                                                                                RANK
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97US-0064671
96US-0059978
                                          97WO-US23775
                                                                                                                                                                                                                          partial sequence encoded by cDNA clone 9D-15C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -QGPSTRPVEV---PGGRAVAAILGLGL-VLGLLGPLAILLALYLLR--
                                                                                                                                                                                                                                                                                                                   Protein;
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07-MAR-1997;

97US-0813509

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AAW6822
XX AAW682
XX AAW682
XX AAW682
XY 08-OCT
XX DE RANK P
XX RANK;
KW Immuuee
KW RANKL;
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC This represents a partial sequence of the polypeptide RANK (receptor CC activator of necrosis factor-kappab (NF-kB)). RANK is a member of CC the tumour necrosis factor family. A soluble RANK may be used for CC inhibiting activation of NF-kB, by contacting a cell expressing membrane CC associated RANK with a soluble RANK which binds to RANK ligand (RANKL). CC RANKL polypeptides can activate RANK and can be used to induce maturation CC admitted cells and enhance their allo-stimulatory capacity, thereby CC augmenting an immune response. The soluble RANK polypeptide composition CC may also be used for regulating an immune or inflammatory response. CC Inhibition of NF-kB by RANK antagonists may be useful in amaliorating CC negative effects of an inflammatory response that result from triggering CC of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host creactions, or acute inflammatory reactions. They can also be used in CC adjunct therapy for disease characterised by neoplastic cells that CC express RANK. RANKL polypeptides can also be used in the content of the strength of the presence of high levels of TWF-alpha. The products can also be used for the presence of high levels of TWF-alpha. The products
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Best Local
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                 RANK; necrosis factor-kappa B; NF-kB; receptor activator; human; immune response; inflammatory response; toxic shock; sepsis; RANKL; RANK ligand; tumour necrosis factor; TNF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                  08-OCT-1998
                                                                                                                                                                                                        AAW68287 standard; Protein; 451
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                                                                                          RANK polypeptide partial sequence encoded by cDNA clone 9D-15C.
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                                                                                                                                                                                                                                                                                                  flgkrvehhgteksdavcssslparkppne 206
                                                                                                                                                                                                                                                                                                                                                                       hwsqdcec-crrntecapglgaqhplqlnkdtv-ckpclagyfsdafsstdkcrpwtnct
                                                                                                                                                                                                                                                                                                                                                                                                                                               kctttsdsvclpcgpdeyldswneedkcllhkvcdtgkalvavvagnsttprrcactagy
                                                                                                                                                                                                                                                                                                                                   LAGKHTLQPASNSSDAICEDRDPPATQPQE 178
                                                                                                                                                                                                                                                                                                                                                                                                            --TQDTVCRCRAGTQ-----PLDSYKPGVDCAPCPPGHFSP--GDNQACKPWTNCT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RCSRSQNTVCRPCGPGFYNDVVSSK-PCKPCTWCNL-----RSGSERKQLCTA--
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70; Conservative
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33.3%;
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Pred. No. 1.1e-09;
1; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 451;
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inhibiting
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23-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (RANKL). The soluble RANK polypeptide composition may also be used for regulating an immune or inflammatory response. Inhibition of NF·kB by RANK antagonists may be useful in ameliorating negative effects of an inflammatory response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, or acute inflammatory reactions. They can also be used in adjunct therapy for disease characterised by neoplastic cells that express RANK. The products can also be used for detection and drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This represents a partial sequence of the polypeptide RANK (receptor activator of necrosis factor-kappaB (NF-kB)). RANK is a member of the tumour necrosis factor family. Host cells transformed or transfected with an expression vector comprising the RANK encoding nucleic acid can be used to produce recombinant RANK protein. The soluble RANK may be used for inhibiting activation of NF-kB, by contacting a cell expressing membrane-associated RANK with a soluble RANK which binds to RANK ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated receptor activator of necrosis factor-kappa for, e.g. developing products for regulating an immune on inflammatory response, treating toxic shock or sepsis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-DEC-1997;
                                                                                                                                              119
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          177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MCVGARRLGRGPCAALLLL-----GLGLSTVTGLHCVGDT-YPSNDRCCHECRPGNGMVS 54
                                                                                                                                                                                                                                                                                                                                                                                                          maprarr--rrplfallllcallarlqvalqiappctsekhyehlgrccnkcepgkymss 58
                                                                   LAGKHTLQPASNSSDAICEDRDPPATQPQE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1998-377655/32.
                                                                                                                                                                                                          --TODTYCRCRAGTO-----PLDSYKPGYDCAPCPPGHFSP--GDNQACKPWTNCT 148
                                                                                                                                                                                                                                                                                                                                                 RCSRSQNTVCRPCGPGFYNDVVSSK-PCKPCTWCNL------RSGSERKQLCTA-- 101
flgkrvehhgteksdavcssslparkppne
                                                                                                                                                                                                                                                                              kctttsdsvclpcgpdeyldswneedkcllhkvcdtgkalvavvagnsttprrcactagy 118
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## ALIGNMENTS

REFERENCE AUTHORS TITLE JOURNAL FEATURES BASE COUNT ORIGIN RESULT 1.
ARO48669
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM source JM Unknown.

Unclassified.

E 1 (bases 1 to 1057)

RS Godfrey,W., Buck,D. and Engleman,E.G.

RRS Godfrey,W., Buck,D. and Engleman,E.G.

Receptor on the surface of activated CD

NAL Patent: US 5821332-A 1 13-OCT-1998;
Location/Qualifiers
1. 1057
1. 1057
1. 1057
1. 1057 AR048669 1057 bp Sequence 1 from patent US 5821332. AR048669 GI:5971012 DNA CD4.sup.+ linear T-cells: ACT-4 PAT 29-SEP-1999

Score

IJ

Description

Query Match Best Local Similarity

98.7%; 99.8%;

Score 1044.4; DB 6; Pred. No. 1.1e-150;

Length 1057;

08-AUG-2001

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Matches
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Godfrey, W. and Engleman, E.G.
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T-cells

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ammalia; Eutheria; l
(bases 1 to 1034)
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Location/Qualifiers
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//db_xref="GI:91340
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 CCCKGAACACGGTGTGCCGTGCGGGCCGGGCTTCTACAACGACGTGGTCAGCTCCA
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X75962
X75962.1 GI:472957
CX40 antigen.
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Latza, U., Durkop, H., Schnittger, S., Ring
Hummel, M., Fonatsch, C. and Stein, H.
The human Ox40 homolog: cDNA structure,
assignment of the ACT35 antigen
Eur. J. Immunol. 24 (3), 677-683 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (16-DEC-1993) U. La
Institute of Pathology, Hinda
Location/Qualifiers
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                    and Seto, A.
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AB003911

ON Rabbit mRNA for OX40 precursor, partial cds.

N AB003911

AB003911.1 GI:2114107

OX40.

Oxyctolagus cuniculus (sub_species:domesticus, sti
HTLV-1-transformed T cell cell_line:H446 cDNA to i
Oryctolagus cuniculus

Oryctolagus cuniculus

Oryctolagus cuniculus

Oryctolagus cuniculus

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                                                                       Direct Submission
Submitted (14-MAY-1997) Takahiro Isono, Shiga University of Medical Science, Central Research Laboratory; Seta Tsukinowachou, Otsu, Shiga 520-2192, Japan (B-mail:isono@belle.shiga-med.ac.jp, Tel:81-775-48-2308, Fax:81-775-48-2048)
                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctola; 1 (bases 1 to 877)
Expression of OX40 and OX40 ligand HTLV-I-transformed T cell lines
                 genes
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                                                                                                                                                                                                           rtebrata; Euteleostom1; Oryctolagus.
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            tcactgtccagcccactgaagcctggcccagaacctcacagggaccctccacccggcccg 633
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                                                                                                                                                                                                                   CCTGCCCCCAGGGCCACTTCTCCGAGGGCAACAACCGGGCCTGCAGGCCCTGGACCAACT
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                                                     CCACGGCCAGGACTTCCACAGCCTGGCCCAGGACAGCCCAGGGTCCTTCCACACCCCACCT
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TGGAGGCCTCCAAGGGCCCCCAGCTGGCCATTGTCCTGAGCCTGGGCCTGGGCCTGGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sub_species="domesticus"
/db_xxef="taxon:9986"
/cell_line="H446"
/cell_type="HTLV-I-transformed
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/protein_id="BAA20059.1"
/brotef="GI:2114108"
/translation="GLAAALGLALLLLGLLLGAEPRPDCVGDTYPGGDRCCLECQPGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Oryctolagus cuniculus"
/strain="Chbb:HM"
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Pred. No. 3.4e-63;
0; Mismatches 229;
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Submitted (07-FEB-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 10, 2002 this sequence version replaced g1:18642353.
                                                                                                                                                                                                                                                                                                                                                   Chemistry: Dye-terminator ET-amersham; 16% of reads Chemistry
Dye-terminator Big Dye; 83% of reads
Consensus quality: 110490 bases at least Q40
Consensus quality: 110677 bases at least Q30
Consensus quality: 110755 bases at least Q20
Insert size: 110819; sum-of-contigs
Insert size: 160089; 6.7% error; agarose-fp
Quality coverage: 8.36x in Q20 bases; sum-of-contigs Quality
coverage: 5.95x in Q20 bases; agarose-fp
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Sequencing vector: plasmid; L08752; 100% of reads
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Contact: humquery@sanger.ac.uk
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                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                 42986 43085: gap of 100 bp
43086 54937: contig of 11852
54938 55037: gap of 100 bp
55038 67254: contig of 12217
67255 67354: gap of 100 bp
67355 111119: contig of 43765
Location/Qualifiers
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ASE1; HTGS_ACTIVEFIN;

    Project Information

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Primates;
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                                  CATCCAAGAGGAGCAGGCCGACGCCCACTCCACCCTGGCCAAGATCTGACC-TGGGCCCA
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Pred. No. 4.5e-51;
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                                                                                                                                                                                                                                                                                                                                                                       * NOTE: This is a 'working draft' sequence. It currentl
* consists of 29 contigs. The true order of the pieces
* is not known and their order in this sequence record
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----- Project Informa
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PROGRESS ***
                                                                                                                                                                                                                                                                                           * arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* This record will be updated and the accession number will
* as soon as it is available and the accession number will
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Mammalia; Eutheria;
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be preserved.
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chromosome 1 clone RP11-465B22,
, 29 unordered pieces.
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* 150848 154411: contig of 3564 bp in length

154412 154511: gap of 100 bp

* 154512 180672: contig of 26161 bp in length

180673 180772: gap of 100 bp

180773 187118: contig of 6346 bp in length

187119 187218: gap of 100 bp

187219 197762: contig of inc.
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63265 63267: contig of 2293 bp in length
63265 69307: contig of 6043 bp in length
63266 69407: gap of 100 bp
69408 76647: contig of 7240 bp in length
76648 76747: gap of 100 bp
76748 98297: contig of 7150 bp in length
98298 98397: gap of 100 bp
98398 100781: contig of 21550 bp in length
100782 100881: gap of 100 bp
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206862: contig of 3331 bp
6962: gap of 100 bp
210944: contig of 3982 bp
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                                 δõ
                                                                                            Query Match 36.8%;
Best Local Similarity 76.2%;
Matches 609; Conservative
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FEATURES

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ORIGIN	BASE COUNT 38968	misc_feature	misc_feature	misc_feature		misc_feature		misc_feature		misc_feature	Ė	misc_feature		misc feature	ď	misc_feature	ļ	misc feature	1	misc_feature		misc_feature		misc_feature		misc_feature		misc_feature		misc_feature		misc_feature		misc_feature		misc_feature		misc_feature		misc_feature		mrsc_reacure
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447 accaactgcaccttggctgggaagcacaccctgcagccggccagcaatagctcggacgca 506 Score 389.8; DB 2; Pred. No. 3.8e-51; 0; Mismatches 2; Length 210944; Indels 188; Gaps

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TITLE The human OX40 homolog: cDNA structure, expression and chromosomal assignment of the ACT35 antigen JOURNAL Eur. J. Immunol. 24 (3), 677-683 (1994) MEDLINE 94170844	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; CE 1 (bases 1 to 5150) RS Latza, U., Durkop, H., Schnittger, S., Ringeling, J., Ei Hummel, M., Fonatsch, C. and Stein, H.	GI:8926701 gen; OX40 gene; rat OX40 antige y Metazoa; Chordata; Craniata; V.		370	980 gatggctgcctccggctctc 	QY       920       caggtgcaggcctgcccgccacgctcctgggccaactctgcaccgttctaggtgcc       979	Qy 860 ccaaggtggacgctgggccccgccaggctggaggcccggagggtctgctgggggagcaggg 919	Qy 800 catccaagaggagcaggccgacgcccactccaccctggccaagatctgaccttgggccca 859	Qy 777 799    III	Oy 758 cgatgcccacaagccccct776	QY       698       gggcccctggccatcctgctggccctgtacctgctccggagggaccagaggctgcccc       757	Oy 648gccgtgcggttgccgccatcctgggcctggtgctggtgctgct 697	OY 648 647  Db 8831 CGAATAGGAGAGGGGGGGGCGCATGGGGGCCCCTCCTGTGGACCCCAGCCAG	Qy         627 cggcccgtggaggtccccgggg	Qy 567 aggcccatcactgtccagcccactgaagcctggcccagaaccttcacagggaccctccacc 626	Db 8591 AACAGCTGCACCTTGGCTGGGAAGCACCCCTGCAGCCAGC
exon 3590. 3718 /gene="0x40" /number=6 intron 3719. 3796	e . e	intron 27843283 /gene="ox40" /number=4 exon 32843480	/gene="0x40" /number=3 exon 27172783 /gene="0x40" /number=4	/number=2 2328. 2429 /gene="ox40" /number=3 intron 2430. 2716	/gene- /number on 1758.	intron 14381634 /gene="ox40" /number=1 /number=1	QDTVCRCRAGTOPLDSYR VK.PK-GEFGE I NDV VSSAK-C.R-C.IN-CREAD-SERROLL-LAI QDTVCRCRAGTOPLDSYR FGVDCAFCEPGHESSEGDNQACKPMTGTLAGKAN SSDAICEDRDPPATOPOETOGPPARP ITVOPTEAMPRTSOGPSTRPVEVPGGRAVAAI LGLGLVLGLLGPLAILLALYLLRRDORLPPDAHKPPGGGSFRTPIQEEQADAHSTLAK I"	/product correction and regen /proteth_id="CAB96543" /db_xref="GI:8926702" /db_xref="GI:8926702" /translation="MCVGARRLGRGPCAALLLLGLGLSTVTGLHCVGDTYPSNDRCCH /translation="MCVGARRLGRGPCAALLLLGLGLSTVTGLHCVGDTYPSNDRCCH	homologue	/gene=" /number join(12	20	mRNA join(1267. 1437,16351757,23282429,27172783, 32843480,35903718,37974096)  /gene="ox40" gene 12674096	Location 15150 /organis	JOURNAL Submitted (28-MAR-2000) Pankow R., Inst. of Immunology, FU Berlin, University Hospital Benjamin Franklin, Hindenburgdamm 30, 12200 Berlin, GERMANY Berlin, GERMANY Related sequence X75962	NE 20318724 DE 3 (bases 1 to 5150) RS Pankow,R.	2 Pan and The exp

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76.1%;
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Pred. No. 1.7e-50;
0; Mismatches 3
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REFERENCE
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TITLE
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KEYWORDS
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                              Barclay, A.N.
Direct Submission
Submitted (27-OCT-1989) Barclay A. N., MRC Cellular Immu
Submitted (27-OCT-1989) Barclay A. N., MRC Cellular Immu
Unit, Sir William Dunn School of Pathology, South Parks
Oxford OX1 3RE, U.K

2 (bases 1 to 1017)
Mallett, S., Fossum, S. and Barclay, A.N.
Characterization of the MRC OX40 antigen of activated CD
T lymphocytes-a molecule related to nerve growth factor
EMBO J. 9 (4), 1063-1068 (1990)
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Mammalia; Eutheria;
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like cysteine rich repeat
                                                           cysteine rich repeat
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Sciurognathi; Muridae; Murinae;
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                                                                                    CATCCATGTGAGACTGGCTTCTACAATGAAGCTGTCAATTATGATACCTGCAAGCAGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 883)
Calderhead, D.M.
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/clone="pUCOx40.RJ.1"
/cell_line="TH2 D.10"
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/strain="Balb/c"
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Pred. No. 5.7e-48;
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                           gagtgcaggccaggcaacgggatggtgagccgctgcagccgctcccagaacacggtgtgc
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cgtccgtgcgggccgggcttctacaacgacgtggtcagctccaagccgtgcaagccctgc
                                                                                     tch 27.1%;
al Similarity 66.6%;
428; Conservative
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Sequence 10
AR019521
AR019521.1
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Baum, P. R., Fanslow, W. C. III, Gayle, R.B.
Cytokine which is a ligand for OX40
Patent: US 5783665-A 10 21-JUL-1998;
                                                                                                                                                                                                              Unknown.
Unclassified.
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CATCCGTGTGAGACTGGCTTCTACAATGAAGCTGTCAATTATGATACCTGCAAGCAGTGT
          cgtccgtgcgggccggggcttctacaacgacgtggtcagctccaagccgtgcaagccctgc
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428; Conser
                                                                                                                                                                                                                                                                                                                                          I14936
Sequence 1
I14936
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Baum, P.R., Fanslow, W.C. III, Gayle, R.B. and Cytokine which is a ligand for OX40
Patent: US 5457035-A 10 10-OCT-1995;
Location/Qualifiers
1. .1317
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                                                                                                                                                         JM Unknown.

Unclassified.

Unclassified.

E 1 (bases 1 to 618)

AS Baum, P.R., Fanslow, W.C. III, Gayle, R.B. an Cytokine which is a ligand for OX40 Cytokine which is a ligand for OX40 Location/Qualifiers

Location/Qualifiers

1.618

1.618
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                            GAGTGCCAGGCCATGGTATGGTGAACCGCTGTGATCATACCAGGGATACTCTATGT
                                                                                     ACACAGTGCAACCATCGAAGTGGAAGTGAACTCAAGCAGAATTGCACACCTACTCAGGAT
        acgtggtgtaacctcagaagtgggagtgagcggaagcagctgtgcacggccacacaggac
                                                                 gagtgcaggccaggcaacgggatggtgagccgctgcagccgctcccagaacacggtgtgc
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Sequence 6
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3.4e-34;
hes 158;
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l (bases 1 to 618)
Baum, P.R., Fanslow, W.C. III, Gayle, R.B.
Gytokine which is a ligand for 0x40
Patent: US 5457035-A 6 10-0CT-1995;
Location/Qualifiers
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Pred. No. 3.4e
0; Mismatches
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5457035.
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3.4e-34;
nes 158;
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AUTHORS
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SOURCE
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DEFINITION
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Search completed: June 18, Job time: 14967 sec
                                                                                                                                                                                                                                                                                                 Query Match 11.8%;
Best Local Similarity 74.8%;
Matches 169; Conservative
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                                                                                 1012 ccatgcatacctcctgccccgcgggaccacaataaaaaaccttggca 1057
                                                                                                                                                                                   6021 ACCCGAAAAATCTACTAAACGAACAAAACAAATACAAACCGCCTACCCCGCCACGCTCCT 5962
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                                                                  CCATACATACCTCCTACCCCGCGAAACCACAATAAAAACCTTAACA 5856
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Patent: WO 0168912-A 304 20-SEP-2001;
Epigenomics AG (DE)
Location/Qualifiers
1. 6080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         artificial sequence.

1 (bases 1 to 6080)

Olek,A., Piepenbrock,C. and Berlin,K.

Diagnosis of diseases associated with tumor suppressor genes and
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Sequence 304 from Patent W00168912.
AX251336
AX251336.1 GI:15984759
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synthetic construct
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                                                                                                                                                                                                                                                                                                                                                                                  /organism="synthetic construct"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
278 c 1963 g 2715 t
           2002,
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Pred. No. 3.7e-10;
0; Mismatches 56;
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Perfect score:
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) BF063899
h BI911081
BE349098
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AI452801
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AI991307
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Compugen Ltd
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Million cell updates/sec
       AI738634 willdO2.x
BI833441 603088095
BG238062 naf22a07.
BF063899 7h90a10.x
BI911081 603069733
BE349098 ht509055.x
AAW293499 UI-H-BI2-AAP91207 wu42d05.x
AA970291 0p09h05.x
AA970291 0p09h05.x
AA970291 0p09h05.x
AA936055 EST177040
AA501118 vf97h05.r
AI323390 mp61a10.x
AI91208 wd76e10.x
AI91208 wd76e10.x
AI912208 wd76e10.x
AI912208 wd76e10.x
AI912208 wd76e10.x
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5.7	5.7	5.7	5.7	5.7		5.7		5.8		6.0								6.7			7.7	8.1	8.7	•		12.8	13.1
1101	1100	817	613	978	724	691	911	1389	1137	313	885	1203	935	932	776	888	935	925	1389	925	459	414	92	459	423	511	560
12	12	12	12	12	12	12	12	10	10	9	12	12	12	12	12	12	12	12	10				_			10	9
CNS01523	AG161988	AG140822	AG043036	AG030617	AG171201	AG171171	AG043617	BG624255	BG809979	BB164410	AG159162	CNS015Y4	CNS006XK	CNS0072Q	CNS010RY	AG030591	CNS006XK	CNS0091P	BG624255	CNS0091P	AW744325	BE095512	BI821828	AI323199	AA110765	BM285756	AW743856
AL104901 Drosophil	AG161988 Pan trogl	Pan	Pan	-	Pan	Pan	AG043617 Pan trogl	BG624255 CVEMB-196	BG809979 mgct002xd	BB164410 BB164410			AL066051 Drosophil		AL099352 Drosophil	AG030591 Pan trog1	AL066051 Drosophil		BG624255 CVEMB-196	AL053013 Drosophil	AW744325 ur30h11.y	BE095512 UI-R-BU0-	ന		AA110765 mp61a10.r	BM285756 524474 MA	AW743856 ur30h11.x

## ALIGNMENTS

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KEYWORDS
SOURCE
ORGANISM
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AI738634/c
LOCUS
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                                                                                                                         source
                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              willd02.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2389923 3' similar to SW:OX40_HUMAN P43489 OX40L RECEPTOR PRECURSOR ;contains MER22.t3 MSR1 repetitive element ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                   Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 844)
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National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI738634.1 GI:5100615
/tissue_type="colon tumor, RER+"
/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="IMAGE:2389923"
/clone_lib="NCI_CGAP_Co16"
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                                                                                                                                                              catgcatacctcctgccccgcgggaccacaataaaaaccttggcag 1058
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mRNA sequence.
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603088095F1 NIH_MGC_120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Subtraction by Bento Soares and M. Fatima Bonaldo.
                GI:15944991
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93.6%;
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Pred. No. 3.4e-98;
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                                                          clone IMAGE: 5227199
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Clone distribution: MCC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11571 row: m column: 24
High quality sequence stop: 659.
Location/Qualifiers
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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National Institutes of Health, Mammalian
Unpublished (1999)
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/db_xref="taxon:9606"
/clone="IMAGE:5227199"
/clone_lib="NIH_MGC_120"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-Torgan: pooled pancreas and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Grüber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."
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95.2%;
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naff2a07.x1 Soares_NPBMC F
similar to SW:OX40_HUMAN F
MER22.tl TAR1 repetitive e
BG236062
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High quality sequence stop: 478.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissue Procurement: M. Bento Soares, cDNA Library Preparation: M. Bento :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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Unpublished (1997)
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Mammalia; Eutheria;
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National Cancer Institute, Cancer Genome Ana
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                    Similarity
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      Conservative
                                                                                                Soares (
                                                                                                                                            /clone_lib="Soares_NPBMC"
/tissue_type="lymphocyte"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: blood; Vector: pT7T3D-Pac; S
Site_2: EcoRI; 1st strand cDNA was primed
oligo(dT) primer [57
                                                                                             is normalized; constructed in the laboratory of M. Bento Soares (University of Iowa)."

179 c 223 g 89 t
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/db_xref="taxon:9606"
/clone="IMAGE:4141716"
                    51.0%;
99.8%;
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Primates;
     0
   Score 540; DB 10;
Pred. No. 5.2e-85;
0; Mismatches 0;
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Homo since IMAGE:4141716 3'
P43489 OX401 RECEPTOR PRECURSOR ;contains
element ;, mRNA sequence.
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                              cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing C
Clone distribution: NCI-CGAP clone distribution information
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@inage_llnl.gov
Seq_primer: -40UP from Gibco
                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae 1 (bases 1 to 544)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Pro
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                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D.,
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603069733F1 NIH_MGC_118 Homo
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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38; Conservative
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//organism="Homo sapiens"
//db_xerf="taxon:9606"
//dlone='IMAGE:332326"
//clone='IMAGE:332326"
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//tasue_type="colon tumor, RER+"
//tasue_type="colon tumor, RER+"
//tasue_type="colon: Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
plasmid DNA from the normalized library NCI_GAP_CO10 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1057416-1061255, and 1144584-1145351).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
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0; Mismatches 1;
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
blate: LLAM11549 row: b column: 10
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High quality sequence stop: 593.
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D., CDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, T
I.M.A.G.E. Consortium DNA Sequencing by: Washington Universit
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information
found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 512)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 314)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            info@image.llnl.gov
Seq primer: -40UP from Gibco
                                                                                                                                               Similarity
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                                                                                                                              Conservative
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                                                                                                                                                                                                                                        /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Sal1. Site_2: Not1; Cloned unidirectionally. Primer: Oligo Library constructed by Life Technologies."

162 c 200 g 77 t
                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ITMAGE:3159200"
/clone_lib="NCI_CGAP_Mell5"
/tissue_type="malignant melanoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                /lab_host="DH10B"
                                                                                                                                             46.8%;
                                                                                                                                               Score 495; DB 10;
Pred. No. 3.8e-77;
                                                                                                                              Mismatches
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UI-H-B12-ahg-a-02-0-UI.sl NCI_CGAP_Sub4 Homo sapiens cDNA clone
IMAGE:2727458 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
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/clone="IMAGE:2727458"
/clone="IMAGE:2727458"
/clone="Iba"NCI_CGAP_Sub4"
/lab_host="bH10B (Life Technologies)"
/lab_h
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Best Local Similarity
Matches 431; Conserv
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ATAAAAACCTTGGCAG
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NCI_CGAP_Kid3 pool 1: LLAM 334-333, 3682-3683, 3798-3802; (IMAGE CloneIDs 1322375-1322911, 1456008.1456775, 1500552-1505255) NCI_CGAP_Kid5 pool 1: LLAM 338-3342, 3722-3725, 376-3778 (IMAGE CloneIDs 1323912-132581), 147136-147293, 149204-1493255) NCI_CGAP_Kid5 pool 1: LLAM 3757-3582, 3851-3854 (IMAGE CloneIDs 1414920-1417991, 1520904-1522439) NCI_CGAP_GC4 pool 1: LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE CloneIDs 1323912-3725, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 376-3729, 3
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                                               atgcccacaagccccctgggggaggcagtttccggacccccatccaagaggagcaggccg
                                                                                                    ATGCCCACAAGCCCCCTTGGGAGGCAGTTTTCCGGGGCCCCCATCCAAAAAGGAGCAGGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 797 Std Error: 0.00
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EST.
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1 (bases 1 to 668)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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h quality sequence stop: 217.
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                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2522697"
/clone_lib="Soares_Dieckgraefe_colon_NHCD"
/tlssue_type="colonic mucosa from 3 patients with Crohn's disease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                   33.3%;
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Pred. No. 3.4
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                                                                           GCAATCCTGCTGGCCCTGTACCTGCTCCGGAGGGACCAGAGGCTGCCCCCCGATGCCCCAA
 CAAGACCCCTGGGGGAGGCAGTTTCCGGACCCCCATCCAAGAGGAGCAGGCCGACGCCAA
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1 (bases 1 to 398)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D.,
Emmmert-Buck, M.D., Ph.D.
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similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Stratagene, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST.
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Seq primer: -40ml3 fwd. ET from Amersh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                        /tissue_type="kidney tumor"
/lab_host="SOUR (kanamycin resistant)"
/note="Organ: kidney; Vector: Bluescript SK-; Site_1:
ECORI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Pooled kidney tumors. 5' adaptor sequence: 5'
GAATTCGGCACGAG 3' 3' adaptor sequence: 5'
CTCGACTTTTTTTTTTTTTTTTTTTTT 3' Average insert size: 1.0 kl
a 125 c 146 g 66 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="NCI_CGAP_Kid6"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:1575225"
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SW:OX40_HUMAN
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94.0%;
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Pred. No. 1.3e-48;
0; Mismatches 19;
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Homo sapiens cDNA clone IMAGE:1575225 3'
P43489 OX40L RECEPTOR PRECURSOR;, mRNA
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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UI-H-BI2-agd-b-03-0-UI.S1 NCI_CGAP_Sub4 Homo sapiens cDNA clone
IMAGE:2723669 3', mRNA sequence.
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National Cancer Institute, Cancer Genome Anat
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            Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: coppbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                            tj50f10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens IMAGE: 2144971 3' similar to contains MER22.t3 MER22
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                       1035 ggaccacaataaaaaccttggcag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          gtgccgatggctgcctccggctctctgcttacgtatgccatgcatacctcctgccccgcg
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                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGCCGATGGCTGCCTCCGGCTTTTTGCTTACGTATGCCATGCATACCTCCTGCCCCGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGGAGGGACCAGAGGNTGCCCCCCGATGCCCACAAGCCCCCTGGGGGAGGCAGTTTCCGG
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 393)
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., Whi
                                                                                                                                                                                                                          AA306055 393 bp mRNA linear EST177040 Jurkat T-cells VI Homo sapiens cDNA 5' 6
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                                                                                                                                              EST.
                                                                                                      Homo sapiens
                                                                                                                           human.
                                                                                                                                                               AA306055.1 GI:1958383
                                                                                                                                                                                                       similar to OX40 homolog, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Another Porgan: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized Libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NbHSF pool 1: 309384-310919, 323208-32895 Soares NbHSF pool 1: 150407, 151176-152327 Soares NbHSF pool 1: 758280-760583, 772104-774407 Soares NbHPA pool 1: 758280-760583, 772104-774407 Soares NbHPA pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatina Bonaldo." 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51
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/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 298.2; DB 9;
Pred. No. 8.6e-43;
0; Mismatches 9;
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RESULT 1
AA501118
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                                                                                                                                                                                                                                                                                                     GGCTGGGAAGCACCCTGCAGCCGGCCAGCAATAGCTCGGACGCAATCTGTGAGGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ggctgggaagcacaccctgcagccggccagcaatagctcggacgcaatctgtgaggacag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCAGGGCACTTCTCCCCAGGCGACAACCAGGCCTGCAAGCCCTGGACCAACTGCACCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | tecagggcacttcttcccaggcgacaaccaggcctgcaagccctggaccaactgcacctt 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald, L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., De B. M., Marmaros,S.M., Merrick,J.M., Morrick,J.M., De B. M., Marmaros,S.M., Merrick,J.M., Morrick,J.M., Merrick,J.M., Me
AA501118 630 bp mRNA linear EST 01-JUL-1997 vf97h05.rl Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:851769 5' similar to gb:Z21674 M.musculus Ox40 (MOUSE);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96026280
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/clone_lib="Jurkat T-cells VI"
/cell_type="T-lymphocyte"
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/db_xref="ATCC (inhost):160207"
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  189
                                           384
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                                                                                                                                                                                                         270 tggtgtaacctcagaagtgggagtgagcggaagctgtgcacggccacacaggacaca 329
                                                                                                                                                                                                                                                                                                       210 ccgtgcgggccgggcttctacaacgacgtggtcagctccaagccgtgcaagccctgcacg
                                                                                                                                                                                   69
                                                                                                                                                                                                                                                                               9
GACTGTGTTCCCTGCCCTCCTGGCCACTTTTCTCCAGGCAACACCCCAGGCCTGCAAGCCC
                        GTCTGCAGATGTAGACCAGGCACCCAACCTCGGCAAGACAGCGGCTACAAGCTTGGAGTT
                                                                                                                 | 9tctgccgctgccgggcgggcacccagcccctgga-----cagctacaagcctggagtt
                                                                                                                                                                                   CAGTGCAACCATCGAAGTGGAAGTGAACTCAAGCAGAATTGCACACCTACTCAGGATACT 128
                                                                                                                                                                                                                                                                             CAGGGTGAGACTGGCTTCTACAATGAAGCTGTCAATTATGATACCTGGCAGCAGTGTACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1996)
Contact: Marra M/Mouse EST Project
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 196.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:851769"
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  with a modified polylinker; Site_1: Not I; Site_2: Eco
  RI; 1st strand cDNA was primed with a Not I - oligo(dT)
  primer [5'
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/dev_stage="4 weeks"
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AI323590
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                                                                                                                                                                                                                                                                 Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 609)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HHMI Mouse EST Project
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Mammalia; E
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                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                              clone was previously sequenced
is from the 3' end
quality sequence stop: 456.
location/Qualifiers
                          /organism-"Mus musculus"
/strain="C57BL/6J"
/db_xref-"taxon:10090"
/clone-"IMAGE:573690"
/clone-1ib-"Soares_thymus_2NbMT"
/sex="male"
/tissue_type="Thymus"
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EST.
Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Verte Eukaryota; Metazoa; Chordata; Catarrhini; Hom Mammalia; Eutheria; Primates; Catarrhini; Hom 1 (bases 1 to 247)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                       AI914208
wd76e10.xl NCI_CGAP_Lu24
                                                                                                                                             mRNA sequence.
                                                                                       human.
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100 thers
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/lab_host="DH108"
                                                                                                                  GI:5634063
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                                                                                                                                                          Homo
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o sapiens
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  Anatomy Project (CGAP),
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IMAGE:2337546 3',
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Tumor Gene Index

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Search completed: June 18, 2002, 17:56:27 Job time: 12105 sec
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Best Local Similarity 96.9
Matches 221; Conservative
                                                                                                     source
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                                                                                                                                                                                                                                                                               831 accotggccaagatotgacottgggcccaccaaggtggacgctgggccccgccaggctgg 890
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                                                                                                                                                                                              cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 373 Std Error: 0.00
Seq primer: -40UP from Gibco.
Location/Qualifiers
1. .247
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon.9606"
/clone="IMAGE:2337546"
/clone="IMAGE:2337546"
/clone=lib="NCI_CGAP_LU24"
/tissue_type="carcinoid"
/lab_bost="PH10B"
/lab_host="PH10B"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_LU5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs l141920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41
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Result
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Perfect score:
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Copyright (c) 1993 - 2000 Comp
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6360.946 Million cell updates/sec
                                      ACT-4 cell surface
ACT-4 h-1 receptor
Human Ox-40 cDNA.
Plasmid pDC406/Ox4
Ox40/Fc cDNA. Syn
Mouse type-II memb
Mouse Ox40 extrace
                                                                                                                                                                                                                  Description
Tumour suppressor Oligonucleotide fo
  AAQ88758
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## ALIGNMENTS

Cell surface receptor; ACT-4; T-lymphocyte; T-cell; immune system; (BECT ) BECTON DICKINSON CO /\*tag= \(\nu\)
/\*tag= \(\nu\)
1042..1047 93US-0147784 94WO-GB02415 /\*tag= 15..86 Location/Qualifiers a

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Antigen OX-40 is specifically expressed on the cell surface of antigen activated T-cells, especially, for example, CD4+ T-cells. I human CDNA encoding the human OX-40 homologue was cloned as follows Using the Experimental Autoimmune Encephalomyelitis model in rats the OX-40 antigen was identified (expressed on the surface of activated autoantigen-specific CD4+ T-cells present at the site of inflammation but absent on CD4+ T-cells at non-inflammatory sites) and cDNA encoding the antigen was isolated. PCR primers were designed and used to clone murine OX-40 cDNA by PCR from RNA isolated from murine CD4+ T-cells activated with concanavalin A.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                           acattcaggccaaccactgtccaatccaccacagtctggcccaggacttctgagttgccc
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93US-0097827
               95US-0494574
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                                                                                           /note= "changed mutant"
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mutant"
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Best Local Similarity 66.0
Matches 428; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fusion protein that contains the extracellular domain of mouse OX40 fused to the mutated Fc region of the human IgGl antibody. The fusion protein was used for detecting cDNA clones encoding an OX40 ligand. The invention claims for a murine OX40-L cytokine (AAW48975) that binds to the murine T cell antigen, OX40. The OX40-L protein is claimed to be useful for co-stimulation of T-cell production and in binding assays for detecting OX40 or its homologues. The OX40-L protein is also claimed to generate a TH-2 immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Purified polypeptide OX-40 ligands - for co:stimulation production and binding assays for OX-40 and homologues
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DB; AAW48976.
ctggtgctggggctgctggggccccttggccatcctgctggccc
                                                                                                                                                                                                ccctggaccaactgcaccttggctgggaagcacaccctgcagccggccagcaatagctcg
                                                                                                                                                                                                                                                                                                         gttgactgtgccccctgccctccagggcacttcttcccaggcgacaaccaggcctgcaag
                                                                                                                                                                                                                                                                                                                                                                                         acagtctgccgctgccgggcgggcacccagcccctgga----cagctacaagcctgga
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                                                                  tccacccggcccgtggaggtccccggggggccgtgcggttgccgccatcctgggcctgggc
                                                                                                                               ccggccaggccatcactgtccagcccactgaagcctggcccagaacctcacagggaccc
                                                                                                                                                                             gacgcagtctgtgaggacagaagcctcctggccacactgctctgggagacccagcgccct
                                                                                                                                                                                                                                            actgtctgcagatgtagaccaggcacccaacctcggcaggacagcggctacaagcttgga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gagtgccagccaggccatggtatggtgaaccgctgtgatcataccagggatactctatgt
                                               tctacacccaccttggtggagcccagatcttgtgacaaaactcacacatgcccaccgtgc
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Pred. No. 1.5e-43;
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Best Local S
Matches 394
                                                                                                                                                                                                                                                                                                                                                                                                New isolated DNA encoding the OX40 ligand polypeptide - also vectors and host cells, used to produce recombinant ligand used in e.g. prim. T cell culture, to modulate immune response etc.
                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                             glycoprotein
                                                                                                                                                                                                                                                                                                                                                         This sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JUL-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US5457035-A.
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                                                                                                                                                                                                                                                           Local Similarity
mes 394; Conserv
                                                                                                                                                                                                                                                                                                                                                                                               host cells, used n. T cell culture,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                          1995-357992/46.
DB; AAR81881.
          gttgactgtgccccctgccctccagggcacttcttcccaggcgacaaccaggcctgcaag
                                                                                                                                                                                                               acagtctgccgctgccgggcgggcacccagcccctgga-----cagctacaagcctgga
                                                                                              cgtccgtgcgggccgggcttctacaacgacgtggtcagctccaagccgtgcaagccctgc
                                                                                                                                                                      gagtgccagccatggtatggtgaaccgctgtgatcataccagggatactctatgt
                                                                                                                                                                                  gagtgcaggccaggcaacgggatggtgagccgctgcagccgctcccagaacacggtgtgc
g#tgactgtgttccctgccctcctggccactttctccaggcaacaaccaggcctgcaag
                                        actgtctgcagatgtagaccaggcacccaacctcggcaggacagcggctacaagcttgga
                                                                                  acacagtgcaaccatcgaagtggaagtgaactcaagcagaattgcacacctactcaggat
                                                                                                                             catccgtgtgagactggcttctacaatgaagctgtcaattatgatacctgcaagcagtgt
                                                                                                                                                                                                                            accgtgacggggctccactgtgtcggggacacctaccccagcaacgaccggtgctgccac 146
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                                                                                                                                                                                                                                                                                                               618
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                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                             present
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                                                                                                                                                                                                                                                                                                               BP; 148 A; 187
                                                                                                                                                                                                                                                                                                                                            encodes the extracellular domain of OX40, a meperesent on the CD4 positive subset of activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytokine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell surface molecule;
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                                                                                                                                                                                                                                                                                                             C; 151 G; 132 T; 0 other;
                                                                                                                                                                                                                                                          Score 283.2; DB 16;
Pred. No. 6.4e-43;
0; Mismatches 158;
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                           The present sequence represents the mouse OX40 extracellular domain encoding cDNA. The extracellular domain of OX40 is its ligand binding domain. The present cDNA was used in the construction of the chimeric OX40/Fc cDNA (AAV32640). The invention claims for a murine OX40-L cytokine (AAW48975) that binds to the OX40 murine T cell antigen. The OX40-L protein is claimed to be useful for co-stimulation of T-cell production and in binding assays for detecting OX40 or its homologues. The OX40-L protein is also claimed to generate a TH-2
                                                                                                                                                                                                                                                                                                                                                                                          Key
                                                                                                                                                 Purified polypeptide OX-40 ligands production and binding assays for C
                                                                                                                                                                                             WPI; 1998-427099/36
                                                                                                                                                                                                                   Baum
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22-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                             OX40; cytokine; OX40/Fc; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV32640 standard;
                                                                                                                              Example 1; Col 31-32;
                                                                                                                                                                                  P-PSDB;
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                                                                                                                                                                                                                                                                                                                21-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse OX40 extracellular domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV32640;
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06-APR-2000;
07-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; DNA; 6080
                     2000DE-1013847.
2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               gene derived chemically modified
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Pred. No. 6.4e-43;
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Sequence 6080

BP; 1124 A;

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C; 1963 G;

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other

11.8%;

DΒ 22;

Length

6080;

ftp.wipo.int/pub/published\_pct\_sequences

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The invention relates to a nucleic acid comprising a sequence of 18 CC bases, of a segment of chemically pretreated MNA (CP DNA) e.g. with CC bisulphite, of genes associated with tumour suppression and CC oncogenes having a sequence taken from 536 (actually 533 since CC numbers 408, 458 and 500 are missing from the sequence listing) sequences CC (Ss) and sequences complementary to (Ss). The nucleic acid may be a CC peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may CC form part of a set of probes for detecting the cytosine methylation state CC and/or single nucleotide polymorphisms and also to be used in an CC array for analysing diseases associated with CpG dinucleotides e.g. CC cancers and tumours. The probes can also be used in a method for CC angore therapy of existing diseases or the predisposition to specific CC diseases, by analysing cytosine methylations. The parameters may be CC compared to another set of genetic and/or epigenetic parameters, the CC differences serving as basis for diagnosis and/or prognosis events which CC are disadvantageous to patients. The present sequence is one of the CC complementary sequences derived from tumour suppressor genes and CC complementary sequence with even numbered Seq ID numbers are the CC complementary sequence with even numbered Seq ID numbered sequence (e.g. Implementary sequence of the corresponding odd numbered sequence (e.g. Implementary sequence of the corresponding odd numbered sequence (e.g. Implementary sequence of the corresponding odd numbered sequence (e.g. Implementary sequence of the corresponding odd numbered sequence (e.g. Implementary sequence of the corresponding odd numbered sequence (e.g. Implementary sequence of the corresponding odd numbered sequence (e.g. Implementary sequence of the corresponding odd numbered sequence (e.g. Implementary sequence (e.g. Imple
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                                                                              of the printed specification, format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
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                                                                                                                            DЬ
                                                                                                                                            QY
                                                                                                                                                                   Query Match
Best Local Similarity 74.8
Matches 169; Conservative
                     1012
                                                                                                                            6080
5901
                                          5961
                                                                                   6021
                                                                                                       892
                                                                                                                                                 832
                                                              952
CCATACATACCTCCTACCCCGCGAAACCACAATAAAAACCTTAACA
           ccatgcatacctcctgccccgcgggaccacaataaaaaaccttggca 1057
                                                    gggccaactctgcaccgttctaggtgccgatggctgcctccggctctctgcttacgtatg
                                                                                CCCTAACCAAAATCTAACC-TAAACCCACAAAATAAACGCTAAACCCCGCCAAACTAAA
                                                                                                                                        AAACCAACTCTACACCGTTCTAAATACCGATAACTACCTCCGACTCTCTACTTACGTATA
                                                                                                                                                                   Score 124.4;
Pred. No. 4.3e
0; Mismatches
                                                                                                                                                                     0;
                                                                                                                                                                     4.3e-14;
ches 56;
                                                                                                                                                                      Indels
5856
                                                                                                                                                                     1;
                                                                                                                                                                     Gaps
                                                            1011
                                                                                                                            6022
                                                                                 5962
                                                                                                       951
                                                                                                                                                 891
                                          5902
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RESULT 9
AAH24887/c
ID AAH248
XX
AC AAH248
XX
DT 22-AUG
XX
DE Oligon
 Oligonucleotide
                    22-AUG-2001
                                       AAH24887;
                                                         AAH24887
                                                          standard;
                    (first
 for a secondary signalling motif.
                                                          DNA;
                    entry)
                                                          117
                                                          ВP
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RESULT 10
AAH24478/c
ID AAH244
XX
AC AAH244
XX
DT 07-AUG
XX',
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                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      secondary signalling sequences. The specification describes stimulatory primary signalling motifs. Primary motifs are efficient at at mediating immune cell signal transduction, particularly when incorporated in an intracellular signalling domain of a chimeric receptor. The primary signalling motif can be combined in any way so as to achieve the desired level of activation (or inhibition) of a number of secondary messenger cascades. The signalling motifs are useful in therapy and in the manufacture of medicament for treating or preventing disease in humans or animals. They are are useful for treating human patients suffering from infectious diseases e.g. human immunodeficiency virus (HIV) infections, inflammatory/autoimmune diseases such as asthma and eczema, congenital diseases e.g. cystic fibrosis, sickle cell anemia dermatological diseases e.g. secondaries neurological
                 07-AUG-2001
                                                                                   AAH24478
                                                                                                                                                                                                                                                                                                                                                                                                                                          sickle cell anemia, dermatological diseases e.g. psoriasis, neurological diseases e.g. multiple sclerosis, transplant-related disease e.g. organ transplant rejection, graft versus host disease, metabolic/idiopathic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stimulatory primary signalling motif; immune cell; signal transduction; chimeric receptor; inflammatory disease; authima; disease; asthma; eczema; congenital disease; cystic fibrosis; sickle cell anemia; dermatological disease; psoriasis; neurological disease; multiple sclerosis; transplant-related disease; metabolic disease; organ transplant rejection; graft versus host disease; diabetes; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligonucleotides AAH24886-87 were used to construct DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-2000; 2000WO-GB04183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CELL-) CELLTECH CHIROSCIENCE
                                                                                                                                                                                                      795
                                                                                                                                                                                                                                        116
                                                                                                                                                                                                                                                                          735
                                                                                                                                                                        56
                                                                                                                                                                                     acccccatccaagaggagcaggccgacgccactccaccctggccaagatctgacc 850
                                                                                                                                                                                                                                                        cggagggaccagaggctgcccccgatgcccacaagccccctgggggaggcagtttccgg 794
                                                                                                                                                                                                                                        CGGAGGGACCAGAGGCTGCCCCGATGCCCAAAAGCCCCCTGGGGGAGGCAGTTTCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . cytoplasmic signalling protein and chimeric receptor protein, il for treating HIV infection, asthma, eczema, psoriasis, multiple osis, contain non-natural stimulatory primary signalling motif
                                                                                                                                                                        ACCCCCATCC AAGAGGAGCAGGCCGACGCCCACTCCACCCTGGCCAAGATCGGATC
                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fig
                                                                                                                                                                                                                                                                                                           Conservative
               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                             B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; 45pp;
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                                                                                                                                                                                                                                                                                                                                                                                             11
                                                                                   DNA;
                                                                                                                                                                                                                                                                                                                                                                                           ۶.
                                                                                                                                                                                                                                                                                                                          10.5%;
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                                                                                                                                                                                                                                                                                                                                                                                           C;
                                                                                                                                                                                                                                                                                                                                                                                                                             cancer.
                                                                                                                                                                                                                                                                                                      Score 111.2;
Pred. No. 1.1e
0; Mismatches
                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                             45
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                                                                                                                                                                                                                                                                                                                                                                                           26 T;
                                                                                                                                                                                                                                                                                                                           .1e-11;
                                                                                                                                                                                                                                                                                                                                                                                           0 other;
                                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                                                                                                                                                                                           ω.
                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                        Length 117;
                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                   The invention relates to novel primary signalling motifs containing care consensus amino acid sequence. These motifs are extremely efficient at mediating immune cell signal transduction, particularly content at mediating immune cell signal transduction, particularly content at mediating immune cell signal transduction, particularly content at mediating immune cell signal transduction particularly content at medicine and research. Content in content and polypeptides that contain, content are useful in therapy, or in the manufacture of a medicament for content in the content and polypeptides that contain, content are useful in therapy, or in the manufacture of a medicament for content in the content and polypeptides that contain, content in the content and research.

Content in the content in the content and polypeptides that contain and research.

Content in the content in the content in an intent content for the content in the content sequence is one of a large number of oligonucleotides used in the construction of sequence blocks (SBs) of primary and secondary continuation in the content in the con
                                                                                                                                                                                  Query Match
Best Local S
Matches 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acids encoding polypeptides with expanded primary signaling motifs, for use in gene therapy, particularly for treating or preventing infections, inflammations or autoimmune diseases in humans
                                                                                                                                                                                                                                                                                                        Sequence 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; primary signalling motif; sequence block; SB; immunosuppressiv secondary signalling sequence; antinicrobial; antiinflammatory; dermatological; neuroprotective; cytostatic; anti-HIV; antiasthmatic; antisickling; antipsoriatic; antidiabetic; gene therapy; diabetes; immune cell signal transduction; infection; inflammation; cancer; autoimmune disease; congenital disease; psoriasis; neurological disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organ transplant rejection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-2000; 2000WO-GB04193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CELL-) CELLTECH CHIROSCIENCE
                                         795
                                                                                          116
                                                                                                                                         735
56
                                                                                                                                                                                     Local Similarity
nes 113; Conserv
                                                                                     cggagggaccagaggctgcccccgatgcccacaagccccctgggggaggcagtttccgg 794
                   , MH
                                                                                                                                                                                                                                                                                                                                                    impart secondary or le in T cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lawson ADG
                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                        BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; 43pp; English.
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                                                                                                                                                                                                                                                                                                        11 A;
                                                                                                                                                                                                             10.5%;
                                                                                                                                                                                                                                                                                                      35 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       motif SB34 oligo F1340B
                                                                                                                                                                                     0
                                                                                                                                                                                  Score 111.2;
Pred. No. 1.1e
0; Mismatches
                                                                                                                                                                                                                                                                                                        45
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                                                                                                                                                                                                        111.2;
No. 1.1
                                                                                                                                                                                                                                                                                                        26 T; 0 other;
                                                                                                                                                                                                      .le-11;
                                                                                                                                                                                                                                   DB 22;
                                                                                                                                                                                     Indels
                                                                                                                                                                                                                              Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunosuppressive;
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AAH24544 standard; DNA; 117

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                                                                                                                                                                                                        The invention relates to a novel nucleic acid encoding an adaptor CC receptor protein comprising an extracellular ligand-binding domain, a CC transmembrane domain and an intracellular signalling domain. The CC intracellular signalling domain comprises the cytoplasmic portion of at least one adaptor protein, and the extracellular ligand-binding domain CC is not CD8 or a major histocompatibility complex (MHC) class I protein. CC The adaptor receptor protein and the nucleic acid encoding it are useful in therapy. They are useful in the manufacture of a medicament for the CC treatment or prevention of diseases in humans and animals. They are useful in the treatment of infectious diseases (e.g. HIV infection), CC distance of an autolimnune diseases (e.g. HIV infection), CC dermatological diseases (e.g. cystic fibrosis and sickle cell anaemia), CC dermatological diseases (e.g. psoriasis), neurological diseases (e.g.) compenital diseases (e.g. psoriasis), neurological diseases (e.g.) compenity and metabolic/idiopathic diseases such as diabetes and cancer. The present sequence is one of a large number of oligonucleotides used in the construction of sequence blocks (SBs) of primary and secondary signalling motifs transduce either a cc stimulatory or an inhibitory signal, which regulates primary activation of the present receptor (TCR) complex. Secondary signalling motifs impart conditions of the disparet receptor receptor in the present and secondary signalling motifs may be used as
                                                                       Query Match
Best Local S
Matches 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polynucleotide encoding adaptor receptor protein useful for treating human immunodeficiency virus (HIV) infection, asthma, cy fibrosis, multiple sclerosis, organ transplant rejection, diabete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neurological disease; organ transplant rejection; diabetes; cancer; graft-versus-host disease; adaptor receptor protein; sequence block; SB; primary signalling motif; secondary signalling motif; ss.
                                                                                                                                                               Sequence 117
                                                                                                                                                                                                 components of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Finney HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CELL-) CELLTECH CHIROSCIENCE LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune disease; cystic fibrosis; sickle cell anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antisickling; antipsoriatic; neuroprotective; immunosuppressive;
antidiabetic; cytostatic; HIV infection; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human secondary signalling motif SB34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-AUG-2001
   116
                                     735
                cggagggaccagaggctgccccccgatgcccacaagccccctgggggaggcagtttccgg 794
CGGAGGGACCAGAGGCTGCCCCCGATGCCCAAAAGCCCCCTGGGGGAGGCAGTTTCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anti-HIV; antiinflammatory; antiasthmatic; dermatological;
                                                                                          Similarity
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                                                                         Conservative
                                                                                                                                                             BP; 11 A;
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                                                                                                                                                                                               the adaptor receptor
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                                                                                        10.5%;
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                                                                                                                                                             Ç;
                                                                       0;
                                                                                        Score
Pred.
                                                                                                                                                               45
                                                                                                                                                             Ģ
                                                                     Mismatches
                                                                                        111.2;
No. 1.1
                                                                                                                                                             26 T; 0 other;
                                                                                                                                                                                               protein of the
                                                               . 1.1e-11;
. 1.3e-3;
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                                                                                                                                                                                                 invention.
                                                                       Indels
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57
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735

cggagggaccagaggctgcccccgatgcccacaagccccctgggggaggcagtttccgg

Matches

Local Similarity

10.3%;

Score 109.4; Pred. No. 2.3

.3e-11;

DB 22; <u>,,</u>

Conservative

0;

Mismatches

Indels Length

0

Gaps 794

0;

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                                                                                                                                                                                          mediating immune cell signal transduction, particularly when incorporated in an intracellular signalling domain of a chimeric receptor. The primary signalling motif can be combined in any way so as to achieve the desired level of activation (or inhibition) of a number of secondary messenger cascades. The signalling motifs are useful in therapy and in the manufacture of medicament for treating or preventing disease in humans or animals. They are are useful for treating human patients suffering from infectious diseases e.g. human immunodeficiency virus (HIV) infections, inflammatory/autoimmune diseases such as a constant of the cons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      multiple sclerosis; transplant-related disease; metabo organ transplant rejection; graft versus host disease;
                                                                                 such as asthma and eczema, congenital diseases e.g. cystic fibrosis, sickle cell anemia, dermatological diseases e.g. psoriasis, neurological diseases e.g. multiple solerosis, transplant-related disease e.g. organ transplant rejection, graft versus host disease, metabolic/idiopathic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotides AAH24886-87 were used to construct DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel cytoplasmic signalling protein and chimeric receptor protein, useful for treating HIV infection, asthma, eczema, psoriasis, multiple sclerosis, contain non-natural stimulatory primary signalling motif -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chimeric receptor; inflammatory disease; autoimmune disease; ast eczema; congenital disease; cystic fibrosis; sickle cell anemia; dermatological disease; psoriasis; neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligonucleotide for a secondary signalling
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   Sequence 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                              secondary signalling sequences. The specification describes stimulatory primary signalling motifs. Primary motifs are efficient at at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Finney HM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stimulatory primary signalling motif; immune cell; signal transduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-AUG-2001
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                                                         e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Fig 3; 45pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lawson ADG;
      BP;
                                                         diabetes, and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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   25
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   Α.
45 C;
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36 G;
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   11 T; 0 other;
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                                                                                                                                                                                                              these primary signalling motifs are useful in medicine and research. They are useful in therapy, or in the manufacture of a medicament for treating or preventing disease in humans or in animals. These diseases include infections (e.g. HIV (human immunodeficiency virus) infection), inflammatory or autoimmune diseases (e.g. asthma or eczema), congenital diseases (e.g. eystic fibrosis or sickle cell anaemia), dermatological diseases (e.g. psoriasis), neurological diseases (e.g. multiple sclerosis), organ transplant rejection or graft-versus-host disease, or metabolic/idiopathic diseases (e.g. diabetes or cancer). The present sequence is one of a large number of oligonucleotides used in the construction of sequence blocks (SBs) of primary and secondary
                                                                                          signalling motifs. Primary signalling motifs are sequences that transduce either a stimulatory or an inhibitory signal, which regulates primary activation of the T cell receptor (TCR) complex. Secondary motifs impart secondary or co-stimulatory signalling capacity to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel primary signalling motifs containing a consensus amino acid segue. These motifs are extremely efficient at mediating immune cell signal transduction, particularly when incorporated into an intracellular signalling domain of a chimeric receptor. Nucleic solds that encode, and polypeptides that contain, the process of the contain of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acids encoding polypeptides with expanded primary signaling motifs, for use in gene therapy, particularly for treating or preventing infections, inflammations or autoimmune diseases in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-328791/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CELL-) CELLTECH CHIROSCIENCE
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                                                                  impart secondary or le in T cells.
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RESULT 14
AAH24543
The invention relates to a novel nucleic acid encoding an adaptor receptor protein comprising an extracellular ligand-binding domain, a CC transmembrane domain and an intracellular signalling domain. The intracellular signalling domain and the extracellular ligand-binding domain. The cleast one adaptor protein, and the extracellular ligand-binding domain is not CDB or a major histocompatibility complex (MHC) class I protein. The adaptor receptor protein and the nucleic acid encoding it are useful in therapy. They are useful in the manufacture of a medicament for the treatment or prevention of disease in humans and animals. They are useful in the treatment or prevention of diseases (e.g. HIV infection), inflammatory and autoimmune diseases (e.g. asthma and eczema), compenital diseases (e.g. cystic fibrosis and sickle cell anaemia), compenital diseases (e.g. psoriasis), neurological diseases (e.g. cystic fibrosis and sickle cell anaemia), compenital diseases (e.g. psoriasis), neurological diseases (e.g. cystic fibrosis and sickle cell anaemia), compenital diseases (e.g. psoriasis), neurological diseases (e.g. cystic fibrosis and sickle cell anaemia), compenital diseases (e.g. asthma and eczema).

CC disease and metabolic/idiopathic diseases such as diabetes and cancer. The present sequence is one of a large number of oligonucleotides used in the construction of sequence blocks (SBs) of primary and secondary signalling motifs transduce either a stimulatory or an inhibitory signal, which regulates primary activation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel polynucleotide encoding adaptor receptor protein useful for treating human immunodeficiency virus (HIV) infection, asthma, cystic fibrosis, multiple sclerosis, organ transplant rejection, diabetes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autoimmune disease; cystic fibrosis; sickle cell anaemia; psoriasis; neurological disease; organ transplant rejection; diabetes; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antisickling; antipsoriatic; neuroprotective; immunos antidiabetic; cytostatic; HIV infection; inflammation
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99.1%;
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Pred. No. 2.
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RESULT AAA46581 ID AAS ACC AAS XX ACC AAS XXX DT Tum XXX Can Can Can CCC Can and CCC arith CCC a
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06-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                     genes and analysing
                  The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences, and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g.
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Godfrey,W., Buck,D. and Engleman,E.G. Receptor on the surface of activated Patent: US 5821332-A 1 13-OCT-1998;
Location/Qualifiers
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AF3778 Streptomy
AC104150 Homo sapi
AC01877 Oryva sat
AC026583 Homo sapi
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Minimum

Word size Searched:

Maximum

Result No.

Query Match Best Local Sin Matches 1056;

Similarity

83.7%;

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Baum, P. R., Gayle, R. B. III., Ramsdell, J. Sorensen, R. A., Watson, M.L., Seldin, M. Grabstein, K., Alderson, M.R. et, al. Identification of OX40 ligand and prits activities on OX40 receptor Circ. Shock 44 (1), 30-34 (1994)
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Location/Qualifiers
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caggccgcctgccccgccacgctcctgggccaactctgcaccgttctaggtgccgatggc
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                                                                                                                      GAGGCTGCCCCCGATGCCCACAAGCCCCCTGGGGGAGGCAGTTTCCGGACCCCCATCCA
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                                                                                                                                                                  GCTGGGGCTGCTGGGCCCCTGGCCATCCTGCTGGCCCTGTACCTGCTCCGGAGGGACCA
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                                                                                              TGGGCCTGGGGCTGAGCACCGTGACGGGGCTCCACTGTCTGGGGGACACCTACCCCAGCA
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H.Sapiens mRNA for O
X75962.1 GI:472957
X75962.1 GI:472957
OX40 antigen.
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1 (bases 1 to 1358)

Latza,U., Durkop,H., Schnittger,S., Ringeling,J., Eitelbach,F., Hummel,M., Fonatsch,C. and Stein,H.

The human Ox40 homolog: cDNA structure, expression and chromosoma assignment of the ACT35 antigen

Eur. J. Immunol. 24 (3), 677-683 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (16-DEC-1993) U. Latza, FU Berlin, Klinikum Steglitz, Institute of Pathology, Hindenburgdamm 30, 12200 Berlin, FRG Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
/product="0x40 homologue"
/protein_id="CAA53576.1"
/db_xref="GI:472958"
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/db_xref="taxon:9606"
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The HTLV-I tax protein
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1 (bases 1 to 5150)

Latza, U., Durkop, H., Schnittger, S., Ringeling, J., Eitelbach, F., Hummel, M., Fonatsch, C. and Stein, H.

The human OX40 homolog: cDNA structure, expression and chromosoma assignment of the ACT35 antigen
assignment of the ACT35 antigen
                                                                                                                                                                                                                                                        Homo sapiens ox40 gene
AJ277151
AJ277151.1 GI:8926701
CD134 antigen; OX40 gen
                                                                           Pankow, R., Durkop, H.,
                                                                                                         94170844
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for CD134 antigen,
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1267. .1437
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2784. .328
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2717. .27
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3868. .4096
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3930. .4096
                                                                                     /number=6
3719. .3796
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/gene="ox40"
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SSDAICEDRDPPATQPQETQGPPARPITVQPTEAWPRTSQGPSTRPVEVPGGRAVAAI
LGLGLVLGLLGPLAILLALYLLRRDQRLPPDAHKPPGGGSFRTPIQEEQADAHSTLAK
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3284. .3480,3590. .3718,3797. .3867)
/gene="ox40"
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1267. .1292
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/gene="ox40"
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1267. .4096
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join(1267. .1437.1635. .1757,2328. .
join(1267. .1437.1635. .1757. .4096)
3284. .3480,3590. .3718,3797. .4096)
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/gene="ox40"
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3797. .40
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/gene="ox40"
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/gene="ox40"
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/gene="ox40"
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TITLE
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Best Local
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852 tgggcccaccaaggtggacgctgggccccgccaggctggagcccggagggtctgctggcccggcccgcaggcccggagggtctgctggcccgccgccaggccccgccaggccccgagggcccgcaggcccagcccgccaggccccgccaggccccaaggccccaaggccccaaggccccaaggcccagaggcccaggcccgccaggcccaggccca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCGGGACCACAATAAAAACCTTGGCAG
                                                                                            Homo sapiens chromosome 1 clone RP5-902P8, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.
                                  Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
Center project name: dJ902P8
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/gene="ox40"
/evidence=experimental
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1672 c 1755 g
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/citation=[1]
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                           Project Information
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0; Mismatches
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  GCGGGACCACAATAAAAACCTTGGCAG
                     gcgggaccacaataaaaaccttggcag 1058
                                                                                                                    taggtgccgatggctgcctccggctctctgcttacgtatgccatgcatacctcctgcccc 1031
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                                                                                                                                                                                                                                                        TGGGCCCAACCAAGGTGGACGCTGGGCCCCGCCAGGCTGGAGCCCGGAGGGTCTGCTGGGC 21605
                                                                                 TAGGTGCCGATGCCTCCCGCCTCTCTGCTTACGTATGCCATGCATACCTCCTGCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insert size: 110819; sum-of-contigs
Insert size: 160089; 6.7% error; agarose-fp
Quality coverage: 8.36x in Q20 bases; sum-o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coverage: 5.95x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22049
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43086 549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="assembly_fragment:00075
fragment_chain:1"
67355. .111119
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fragment_chain:1"
55038. .67254
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/db_xref="taxon:9606"
/chromosome="1"
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l. .42985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ragment_chain:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42985: contig of 42985 bp in length 1085: gap of 100 bp 54937: contig of 11852 bp in length 1037: gap of 100 bp 10545; contig of 12217 bp in length 1354: gap of 100 bp 111119: contig of 43765 bp in length
                                                                                                                                                                                                                                                                                                                                                           19.6%;
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Pred. No.
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21458
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1.9e-93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300 others
                                                                                                                                                                                                                                                                                                                                                                              Length 111119;
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몽 S 용 õ В ş 밁 õ

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REFERENCE
AUTHORS
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SOURCE
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AL390719
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VERSION
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JOURNAL
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AL390719
AL390719.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator ET-amersham; 2% of reads
Dye-terminator Big Dye; 97% of reads
Consensus quality: 201072 bases at least Q40
Consensus quality: 204266 bases at least Q30
Consensus quality: 204043 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insert size: 208144; sum-of-contlys
Insert size: 227650; 6.6% error; agarose-fp
Quality coverage: 5.63x in Q20 bases; sum-o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: bA465B22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Feb 1, 2002 this sequence version replaced gi:16304463.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTG;
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Homo sapiens chromosome l clone RP11-465B22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown
* This record will be updated with the finished sequence
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----- Project Informa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (24-JAN-2002) Wellcome Trust Sanger Institute, Hinxton
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * NOTE: This is a 'working draft' sequence. It currentl
* consists of 29 contigs. The true order of the pieces
* is not known and their order in this sequence record
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coverage: 5.53x in Q20 bases; agarose-fp
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60772
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30427 43166: contig of 12740 bp in length
43167 43266: gap of 100 bp
43267 47516: contig of 4250 bp in length
47517 47616: gap of 100 bp
47617 51392: contig of 3776 bp in length
                                                                                                        69308
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8189 23213: contig of 1025 bp in length
23214 23313: gap of 100 bp
23214 27220: contig of 3907 bp in length
27221 27320: gap of 100 bp
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27321 27320: contig of 3006 bp in length
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  cont
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18 98397;
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63164: contig of 2293 bp
55 63264: gap of 100 bp
55 69307: contig of 6043 bp
18 69407: gap of 100 bp
18 67647: contig of 7240 bp
18 76747.
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108388 116410 contig of 8023 bp in length 116411 116510: gap of 100 bp 119167 119266: contig of 2656 bp in length 119167 119267 29ap of 100 bp 119267 121683: contig of 2417 bp in length 121684 121783: gap of 100 bp 125416 125515: gap of 100 bp 125516 132751: contig of 3632 bp in length 132752 132851: gap of 100 bp 132852 137874: contig of 5023 bp in length 132852 137874: gap of 100 bp 137875 137974: gap of 100 bp 174740 147749; gap of 100 bp 1750848 150747: contig of 3655 bp in length 150848 154411: contig of 3665 bp in length 154412 154511: gap of 100 bp 16573 180772: gap of 100 bp 1750748 150748: contig of 3646 bp in length 180773 18718: contig of 3646 bp in length 180773 18718: gap of 100 bp 1750762: contig of 6346 bp in length 187762: contig of 100 bp 187763: contig of 
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clone_end:T7
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fragment_chain:2"
69408. .76647
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/db_xref="taxon:9606"
/chromosome="1"
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fragment_chain:2"
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fragment_chain:2"
53265. .69307
                                                                                                                                                                                                                                                                                    /note="assembly_fragment:03852
fragment_chain:2"
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137975. .147659
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76748. .98297
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fragment_chain:6"
197863. 203431
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154512. .180672
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203532. .206862
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150848. .154411
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fragment_chain:5"
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cggagggaccagaggctgccccccgatgcccacaagccccctgggggaggcagtttccgg 794
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Sequence 58
AX134865
AX134865.1
                                                l Similarity
83; Conser
                                                                                                                                                                                                 artificial sequence.

1 (bases 1 to 117)
Finney, H.M. and Lawson, A.D.
Polypeptides with expanded primary signalling motifs
Patent: WO 0132867-A 73 10-MAY-2001;
Celltech Chiroscience Limited (GB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83;
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Finney, H.M. and Lawson, A.D.
Polypeptides with non-natural primary
Patent: WO 0132709-A 58 10-MAY-2001;
Celltech Chiroscience Limited (GB)
Location/Qualifiers
1. 117
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Similarity 100.0%;
                                             7.8%; Score 83; DB llarity 100.0%; Pred. No. 1. Conservative 0; Mismatches
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/db_xref="taxon:33630"
/note="Chimeric receptor construction oligonucleotide
F1340A"
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/db_xref="taxon:32630"
/note="olloonucleotide for chimeric
45 c 36 g 11 t
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AX134866/c
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Matches 78
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Matches 83
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                                                                                                               artificial sequence.

1 (bases 1 to 117)
Finney, H.M. and Lawson, A.D.
Polypeptides with non-natural primary signalling
Patent: WO 0132709-A 59 10-MAY-2001;
Celltech Chiroscience Limited (GB)
Location/Qualifiers
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Sequence
AX135075
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Sequence 59 from Patent
AX134866
AX134866.1 GI:14271354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        artificial sequence.
1 (bases 1 to 117)
Finney,H.M. and Lawson,A.D.
Hybrid adaptor receptors
Patent: WO 0132866-A 88 10-MAY-2001;
Celltech Chiroscience Limited (GB)
 . Similarity
78; Conserv
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ilarity 100.0%;
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                                                              /organism="synthetic construct"
/db_xxef="taxon:32630"
/note="oligonucleotide for chim
35 c 45 g 26 t
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/db_xref="taxon:32630"
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AX134963/c
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AX135076/c
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TITLE
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Best Local Similarity
Matches 78; Conser
Query Match
Best Local Similarity
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1 (bases 1 to 117)
Finney, H.M. and Lawson, A.D.
Polypeptides with expanded primary signalling motifs
Patent: WO 0132867-A 74 10-MAY-2001;
Celltech Chiroscience Limited (GB)
Location/Qualifiers
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Sequence 74 from Patent W00132867.
AX134963
AX134963.1 GI:14271405
                                                                                                                                      Finney, H.M. and Lawson, A.D.
Hybrid adaptor receptors
Patent: WO 0132866-A 89 10-MAY-2001;
Celltech Chiroscience Limited (GB)
                                                                                                                                                                                   artificial sequence.
1 (bases 1 to 117)
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Sequence 89 from Patent W00132866.
AX135076 AX135076.1 GI:14271471
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                                                      /organism="synthetic construct"
/db_xref="taxon:32630"
/note="Adaptor receptor constucted at 1340B"

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/db_xref="taxon:32630"
/note="Chimeric receptor construction F1340B"
                                                                                                                           Location/Qualifiers
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                                                                                                   l Similarity
32; Conserv
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Matches
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                                                                                           TGGGCCCACCAAGGTGGACGCTGGGCCCCGCC
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The human Ox40 homolog: cDNA structure, expression and chromosomal assignment of the ACT35 antigen
Eur. J. Immunol. 24 (3), 677-683 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (16-DEC-1993) U. Latza, FU Berlin, Klinikum Steglitz, Institute of Pathology, Hindenburgdamm 30, 12200 Berlin, FRG Location/Qualifiers
1. .1373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae. 1 (bases 1 to 1358)
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814. .958
959. .1079
1341. .1346
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LGLGLVLGLLGPLAILLALYLLRRDQRLPPDAHKPPGGGSFRTPIQEEQADAHSTLAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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100.0%; Pr
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Baum, P.R., Fanslow, W.C. III, Gayle, P. Cytokine which is a ligand for OX40 Patent: US 5457035-A 6 10-OCT-1995;

Location/Qualifiers
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Z21674.1
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114933
114933.1
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Baum, P.R., Fanslow, W.C. III, Gayle, F
Cytokine which is a ligand for Ox40.

Patent: Us 5783665-A 6 21-JUL-1998;

Location/Qualifiers

1. 618
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 883) Calderhead,D.M., Buhlmann,J.E., van den Eertwegh,A.J., Claassen,E. Noelle,R.J. and Fell,H.P. Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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187 c 151 g
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Sequence
AR019521
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Baum, P.R., Fanslow, W.C. III, Gayle, R.B.
Cytokine which is a ligand for OX40
Patent: US 5783665-A 10 21-JUL-1998;
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94044750
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               Similarity
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2.6%;
nilarity 100.0%;
Conservative 0
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/db_xref="GI:312828"
/db_xref="MGI:104512"
/db_xref="SWISS-PROT:PA7741"
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CRCRPGTOPRODSGYKLGVDCVPCPGHFSGNQACKPWTNCTLSGKGTRHPASDLD
DAVCEDRSLLATILWETGRPTFRPTTVGSTTWAPRTSELPSPPTLVTPEGPAFAVILG
LGLGLLAPLTVLLALYLLRKAWRLPNTPKPCWGNSFRTPIQEEHTDAHFTLAKI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="0x40"
860. .883
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                                                                                 /organism="unknown"
417 c 337 g
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1. .1317
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/db_xref="taxon:10090"
/clone="pUCOx40.RJ.1"
/cell_line="TH2_D.10"
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/strain="Balb/c"
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                                                                                                                                                                                                                                                                                                                      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalla; Butheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 2907)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 1317)
Baum, Panslow, W.C. III, Gayle, R.B.
Cytokine which is a ligand for OX40
Patent: US 5457035-A 10 10-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
I14936
                                                                                                                                                                                                                                                                                                                                                                                                                      M.musculus ox40 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unknown
                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                         2 (bases 1 to 2907)
Birkeland, M.L.
                                                                                                                                                                                                                                                 95255413
                                                                                                                                                                                                                                                                      of rat 0x40 protein
                                                                                                                                                                                                                                                                                    Gene
                                                                                                                                                                                                                                                                                                Barclay, A.N.
                                                                                                                                                                                                                                                                                                         Birkeland, M.L., Copeland, N.G.,
                                                                                                                                                                                                                                                                                                                                                                                  OX40 gene.
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ilarity 100.0%;
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                     join(180. .312,534. .656,1208.
2472. .2591,2680. .2750)
/gene="ox40"
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1. .1317
                                                                                    /organism="Mus musculus"
/db_xref="taxon:10990"
join(<1..312,534..656,1208.
2472..2591,2680..2907)
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; Murinae; Mus
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BASE COUNT
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SOURCE
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AC100470/c
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Mus musculus clone RP23-139J18,
AC100470
AC100470.1 GI:17047876
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 60953)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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                                                   Mus musculus
                                                          house mouse.
                                                                          HTG; HTGS_PHASEO.
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/number=7
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/gene="ox40"
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1759. .2195
/gene="ox40"
/number=4
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/number=3
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/gene="ox40"
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657. .120
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/db_xref="GI:732819"
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/codon_start=1
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LOW-PASS SEQUENCE SAMPLING
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COMMENT
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 60953)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Boukhgalter, B. Anderson, S., Barna, N., Bastlen, V., Boguslavkiy, L., Boukhgalter, B. Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Cocke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zainoun, J., Zembek, L., Zimmer, A. Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus, clone RP23-139J18
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows
                                                                                                                                                                                                                                                                                                                                                                                                                                                   be preserved.
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16220: gap of 100 bp
16917: contig of 697 bg
17017: gap of 100 bp
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27465: contig of
27565: gap of 1
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17727: c
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Direct Submission
Submitted (26-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on Nov 2, 2001 this sequence version replaced gi:16416310.
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18 54419: contig of 702 bp in 1a
20 54519: gap of 100 bp
20 55229: contig of 710 bp in 1a
30 55329: gap of 100 bp
30 55329: gap of 100 bp
30 56023: contig of 694 bp in 1a
24 56123: gap of 100 bp
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49606: gap of 100 bp
50333: contig of 727 bp in length
50433: gap of 100 bp
51151: contig of 718 bp in length
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43083: gap of 100 bp
4309: contig of 726 bp in length
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4434: contig of 725 bp in length
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42162: contig of 676 bp in length
42262: gap of 100 bp
42983: contig of 721 bp in length
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46280: contig of 719 bp in length
880: gap of 100 bp
47104: contig of 724 bp in length
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contig of 698 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 28; DB 2;
; Pred. No. 0.0041;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                               253111 bp
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Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 250604 bases at least Q40 Consensus quality: 251169 bases at least Q30 Consensus quality: 251526 bases at least Q20 Insert size: 252011; sum-of-contigs Insert size: 263925; 8.0% error; agarose-fp Quality coverage: 11.85x in Q20 bases; sum-of-contigs Quality coverage: 11.37x in Q20 bases; agarose-fp Center project name: bM118E21 Center: Sanger Centre Assembly program: XGAP4; version NOTE: This is a 'working draft' sequence. This record will be updated with the finished sequence Summary Statistics Project Information

it is available and the accession number will

vector\_side:left" /note="assembly\_fragment:07355 fragment\_chain:1" /note="assembly\_fragment:05628 fragment\_chain:1 /clone="RP23-118E21" /clone\_lib="RPCI-23" /chromosome="4" /db\_xref="taxon:10090" organism="Mus musculus" location/Qualifiers

124655. .138457 /note="assembly\_fragment:01898
fragment\_chain:2" /note="assembly\_fragment:00235 fragment\_chain:2" /note="assembly\_fragment:04295 fragment\_chain:1" /note="assembly\_fragment:02677 fragment\_chain:2" 124655 120467

/note="assembly\_fragment:00567
fragment\_chain:2"
179139. .210421 /note="assembly\_fragment:00397
fragment\_chain:2" 138558. .179038

밁 οy

/note="assembly\_fragment:00017
fragment\_chain:2" /note="assembly\_fragment:07085 fragment\_chain:2" fragment\_chain: .224019

/note="assembly\_fragment:03553
fragment\_chain:3
clone\_end:T7 224120. ".227775 /note="assembly\_fragment:01289 fragment\_chain:3" 227876. .253111

ector\_side:right" 61670 c 60569 g g 64276 t 1108 others

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PUBMED
REFERENCE
AUTHORS
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AUTHORS
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AF389853
                  FEATURES
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MEDLINE
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Matches 28; Conser
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                                                                                                                                                                                                                                                                                                                                                                              stimilited (VG-1007 2001) (VSA)

St. Philadelphia, PA 19104, USA

* NOTE: This is a 'working draft' sequence. It currently

* consists of 13 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 32449 32548: gap of unknown length

* 32449 32548: gap of unknown length

* 59001 57000: gap of unknown length

* 115351 115450: gap of unknown length

* 115451 118046: contig of 58350 bp in length

* 115451 118046: contig of 5896 bp in length

* 115451 118046: contig of 5896 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 keea,D.R., Li,X., Bachmanov,A.A., Li,S., Chen,Z., Tordoff,M.G.,
Beauchamp,G.K., de Jong,P.J., Wu,C., Chen,L., West,D.B., Ross,D
and Ohmen,J.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 254197)
Li,x., Bachmanov,A.A., Li,S., Chen,Z., Tordoff,M.G., Beauchamp,G.K., de Jong,P.J., Wu,C., Chen,L., West,D.B., Ross,D.A., Ohmen,J.D. and Reed,D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF389853 254197 bp DNA linear HTG 24-JAN-2002 Mus musculus chromosome 4 clone RPCI-23-118E21 strain C57BL/6J, WORKING DRAFT SEQUENCE, 13 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (08-JUN-2001) Monell Chemical Senses
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Reed, D.R., Li, X., Bach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21635547
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183135
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                  Location
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/ 100.0%; Pr
/ 0;
                                                                                                              118146: gap of u
12365: contig
123865: gap of u
124811: contig
124911: gap of u
13252: gap of u
13252: gap of u
154052: contig
154052: contig
154152: gap of u
164152: gap of u
164152: gap of u
164152: gap of u
164152: gap of u
                                    227817: gap of
254197: contig
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                  /Qualifiers
                                                                       gap of unknown length contig of 4522 bp in length
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Pred. No.
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                                                                                                                                               of unknown length
g of 7341 bp in length
of unknown length
lg of 21700 bp in length
lg of 21700 bp in length
of unknown length
of unknown length
of unknown length
lg of 14482 bp in length
                                                                                                                                                                                                                                                                                                                                 of unknown length
g of 2596 bp in length
of unknown length
g of 5619 bp in length
of unknown length
                                    unknown 1
of 26380
                                                                                                                unknown length of 25279 bp in
                                                                                                                                                                                                                                                                                                                 of 946 bp in
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0.0034;
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REFERENCE
AUTHORS
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KEYWORDS
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AUTHORS
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SOURCE
ORGANISM
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AC007905
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                                                                                                                                                                                                                                                                                                   25
                                                                                                                                                                                               SEQUENCE,
AC007905
Kremmidiotis,G., Gardner,A.E., Callen,D.F. and Sutherland,G.R. Direct Submission
Submitted (24-JUN-1999) Cytogenetics & Molecular Genetics, Women's & Children's Hospital, 72 King William Rd, Adelaide, SA 5006,
                                                                                                                                                                                                                                                                                                                                                    ch 2.2%; So 23; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               synthetic construct artificial sequence.
1 (bases 1 to 5148)
0lek,A., Plepenbrock,C. and Berlin,K.
Diagnosis of diseases associated with tumor suppressor
                                                                                                                                                                                                                          Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AX251339
Sequence 307 from Patent
AX251339
                                                                             Kremmidiotis,G., Gardner,A.E., Callen,D.F
Large Scale Sequencing of the Chromosome
                                                              Unpublished
                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                              Homo sapiens
                                                                                                                                                                     AC007905.2 GI:10280722
HTG; HTGS_PHASE2; HTGS_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Epigenomics AG (DE)
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                                                                            Large Scale Sequencing
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                                                  (bases 1 to 104480)
                                                                                                   (bases 1 to 104480)
                                                                                                                                                                                                            JENCE, 35
                                                                                                                                                                                                                                                                                                                                                                                                                                   871
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ilarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="chemically treated genomic DNA (Homo sapiens)" 182\ c 1479\ g 2615\ t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="synthetic construct"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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60035 c 62871 g 67274
                                                                                                                                                                                                          104480 bp chromosome 16q24.3 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .5148
                                                                                                                                                                    HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                       Score 23; DB; Pred. No. 1.9

 Mismatches

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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5148 bp
: WO0168912
                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                            Callen, D.F. and
Chromosome 16 rec
                                                                                                                                                                                                                          clone
                                                                                                                                                                                                                                                                                                                                                                   DB 6
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one RP4-754F23,
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                                                                                                                                                                                                                           WORKING DRAFT
                                                                                                                                                                                                                                     HTG 03-0CT-2000
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COMMENT
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On Sep 23,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the accession number will be preserved.

1 1479: contig of 1479 bp in length
1480: gap of unknown length
1488: 6699: contig of 5212 bp in length
6700: 6707: gap of unknown length
6708: 10905: contig of 4198 bp in length
10918: gap of unknown length
10918: gap of unknown length
10918: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         consists of 35 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    provided by the submittor. This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently
   52181
52188
60027
60034
64700
64707
69137
69144
73348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the finished sequence as soon as it is available
                                                                                                                    48493
49846
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51200
51207
51514
51521
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113857
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                        60033:
64699:
64706:
69136:
69143:
73347:
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51206:
51513:
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48492:
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45611
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24860: contig
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of 933 bp in length
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of 1917 bp in
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of 1247 bp in length
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of 2632 bp in length
unknown length
of 727 bp in length
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of 9108
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of 3423 bp in
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of 4819 bp in
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of 698 bp in le
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                                                                                                                  sig_peptide
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Rabbit mRNA
AB003911
                                                                                                                                                                                                                                                                                                                                                            Submitted (14-MAY-1997) Takahiro Isono, Shiga University of Medical Science, Central Research Laboratory; Seta Tsukinowachou, Otsu, Shiga 520-2192, Japan (E-mail:isono@belle.shiga-med.ac.jp, Tel:81-775-48-2308, Fax:81-775-48-2048)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Cl
Mammalia; Eutheria; Lagomorpha;
1 (bases 1 to 877)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryctolagus cuniculus (sub_species:domesticus, strain:Chbb:HM) HTLV-I-transformed T cell cell_line:H446 cDNA to mRNA.
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                                                                                                                                                                                                                                                                                           Expression of OX40 and OX40 ligand HTLV-I-transformed T cell lines
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/db_xref="taxon:9606"
/chromosome="16q24.3"
/clone="RP4-754F23"
a 28756 c 29631 g 22706
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GMVSRCNRSQDTICHPCEPGFYNEAVNYQACKPCTQCNRRSGSEPQQECTHTRDTVCR
CRPGTQPLNGYKHGVDCAPCPQGHFSEGNNRACRPWTNCTLAGKRTLQPASSISDAVC
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                                              /codon_start=1
/product="0X40 precursor"
/protein_id="BAA20059.1"
/db_xref="GI:2114108"
                                                                                                                                                              /db_xref="taxon:9986"
/cell_line="H446"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82469: gap of unknown length
84166: contig of 1697 bp in length
84173: gap of unknown length
84827: contig of 649 bp in length
84829: gap of unknown length
99511: contig of 14682 bp in length
99518: gap of unknown length
101087: contig of 1569 bp in length
101087: contig of 1569 bp in length
101094: gap of unknown length
103316: contig of 2222 bp in length
103323: gap of unknown length
103323: gap of unknown length
103323: gap of unknown length
104480: contig of 1157 bp in length
                                                                                                                                             /cell_type="HTLV-I-transformed T cell"
                                                                                                                                                                                                              /strain="Chbb:HM"
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                                translation="GLAAALGLALLLLGLLLGAEPRPDCVGDTYPGGDRCCLECQPGY/
                                                                                                                                                                                             /sub_species="domesticus"
                                                                                                                                                                                                                            organism="Oryctolagus cuniculus"
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Lagomorpha; Leporidae; Oryctolagus
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Homo sapiens, clone IMAGE:3050476,
BC002494
                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Benjamin,B., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Mastello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web Aito.
                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at: Series: IRAL Plate: 4 Row: e Column: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (05-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11AO3, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                 This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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324 c 275 g
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/protein_id="AAH02494.1"
                                                                                                                     /tlssue_type="Skin, melanotic melanoma."
/clone_lib="NIH_MGC_20"
/lab_host="DH10B-R"__
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                                                          /codon_start=2
                                                                                                    /note="Vector:
                                                                                                                                                                                     /clone="IMAGE: 3050476"
                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="GI:12803351"
                                                                                                                                                                                                                                                                        ocation/Qualifiers
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Homo sapiens mRNA; cDNA DKF2p434L1226 (from
AL137382
AL137382.1 GI:6807912
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Clone from S
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Bandman,O., Tang,Y.T., Azimzai,Y., Yue,H., Baughn,M.R., Hillman,J.L., Lal,P., Wang,E., Gandhi,A.R., Policky,J.L. and
                                Submitted (15-JAN-2000) MIPS,
                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1632)
Ansorge,W., Wirkner,U., Mewes,H.W., Well,B. and Wiemann,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent: WO 0153469-A 10 26-JUL-2001; Incyte Genomics, Inc. (US)
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                                                Direct Submission
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10 from Patent W00153469
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flgdprilflerfpaaryasrrvgiavlwislitewlwlifterfddrefwwyhesg
yrsgapaqvyhgepsgletgegspsghcwitgaalwpimtalsgvattarsrwvrymp
slayctfllavglsrifilahfphqvlaglitgavlgwlmtpkypmerelsfygltal
almlgtsliywtlftlgldlswsislafkwcerpewihvdsrpfaslsrdsgaalglg
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PCLVLALVPWAVHMFSAQEAPPIHSS"
1 465 c 361 g 324 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/note="Incyte ID No: 1269556CB1"
/note="Incyte ID No: 357 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
, GERMANY
S. Wiemann,
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n clone DKFZp434L1226).
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German Genome Project.

German Genome Project.

German Genome Project.

This clone (DKFZp434L1226) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 1405

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 1405

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 1405

Please contact the RZPD in Berlin.
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Homo sapiens, clone MGC:31975
BC021574
BC021574.1 GI:18204314
MGC.
                                                                                                                                                                  Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticla Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Please contact the RZPD: Ressourcenzentrum, Heu Berlin-Charlottenburg, GERMANY; Email: clone@rz information about the clone and the sequencing
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 40 Row: 1 Collumn: 5 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Direct Submission
Submitted (14-JAN-2002) National Institutes of Health, Mammalian Submitted (14-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Tractitute. 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by EMBL (European Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/db_xref="taxon:9606"
/db_cxref="htaxon:9606"
/clone="DkFZp434L1226"
/clone=lib="434 (synonym: htes3). Vector pSport1; host
DH10B; sites Not1 + Sal1"
/dev_stage="adult"
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/map="16q24.3"
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Search completed: June 19, 2002, 02:21:10 Job time: 3946 sec
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SCETGEGSPSGIGMITGAALWELMTALSSQVANTARSRWVRWDSLAYCTELLAVGLS
RIFILAHFPHQVLAGLIFGAVLGWLAWPPRVPBERELSFYGLTALALMLGTSLIYWTE
TLGLDLSWSISLAFKWCERPEWIHVDSRPFASLSRDSGAALGLGIALHSPCYAQVRRA
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FSAQEAPPIHSS"
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/protein_id="AAH21574.1"
/db_xref="G1:18204315"
/translation="MESTLGAGIVIAEALQNQLAWLENVWLWITFLGDPKILFLFYFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="MGC:31975 IMAGE:4842511"
/tissue_type="Eye, normal, pigmented retinal epithelium"
/clone_lib="NHH_MGC_43"
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/db_xref="taxon:9606"
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BE349098 ht50905.x
AI738634 willd02.x
AA306055 EST177040
AW293499 UI-H-BI2-
AW290885 UI-H-BI2-
BI833441 603088995
AW591834 xx86b03.x
BI821093 603039230
BI911081 603068733
AI452801 tj50f10.x
BI821828 603035715
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AI991207 wu42d05.x
AI991307 wu42d05.x
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                                               CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing C
Clone distribution: NCI-GGAP clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
info@inage.llnl.gov
Seg primer: -40UP from Gibco
High quality sequence stop: 478.
Location/Qualifiers
                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
Bonaldo, Ph.D.
                                                                                                                                                                                                                    Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 569) NCI-CGAP http://www.ncbi.nlm.nih.gov/nclcgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                   BG236062 FIG. 12 PBMC Homo Sapiens CDNA clone IMAGE:4141716 3' similar to SW:0X40_HUMAN P43489 0X40L RECEPTOR PRECURSOR; contains MER22, t1 TAR1 repetitive element; mRNA sequence.
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BG236062.1 GI:12749909
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/db_xref="taxon:9606"
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AA312871 EST1835.9
AI126122 qd77b04.x
AA312871 EST1835.9
AI126122 qd77b04.x
AA477725 zu44f11.s
BF18198 6 CW2-CI017
AI264358 q109f04.x
AI669655 wC12a05.x
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BF725110 bx12c11.y
BG422683 602449189
BF033463 601460214
AL578769 AL524354
AL5278769 AL524354
BB1258768 602970353
BB312775 601149543
BB474767 60761457833
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BM042047 603616648
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AL526414 AL526414
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BG474551 602517325
AL523389 AL533389
AL524354 AL524357
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544 bp mRNA linear EST 16-OCT-2000 7h90a10.x1 NCI_CGAP_CO16 HOMO Sapiens cDNA clone IMAGE:3333226 3' similar to SW:OX40_HUMAN P43489 OX40L RECEPTOR PRECURSOR ;contains MER22.tl PTR5 repetitive element; mRNA sequence.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
Contact: Robert Strausberg, Email: cgapbs-r@mail.nih.gov
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1 (bases 1 to 544)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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Seq primer: -40UP from Gibco
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-*Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_COlO was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1057416-1061255, and 1144584-1145351). Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="colon tumor, RER+"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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Pred. No. 1.8e-173;
0; Mismatches 0;
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                    ctccggagggaccagaggctgccccccgatgcccacaagccccctgggggaggcagtttc
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                                                                                                                                                                                                   cagggaccctccacccggcccgtggaggtccccggggggccgtgcggttgccgccatcctg
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CTCCGGAGGGACCAGAGGCTGCCCCCGATGCCCACAAGCCCCCTGGGGGAGGCAGTTTC
                                                                                       GGCCTGGGCCTGGTGCTGGGCCTGGGCCCTGGCCATCCTGCTGGCCCTGTACCTG
                                                                                                                                                                                                                                                                                                                                               506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.

Email: cgapbs r@mail.nih.gov

Insue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life

Technologies, Inc. cDNA Library Arrayed by: Christa Prange,

I.M.A.G.E. Consortium DNA Sequencing by: Washington Univers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq
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Clone distribution: NCI-CGAP clone distribution information
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalla; Eutheria; Primates; Catarrhin; Hominidae;
1 (bases 1 to 512)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies."
162 c 200 g 77 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3150200"
/clone_lib="NCI_CGAP_Mel15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="malignant melanoma, metastatic to lymph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-GAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 844)
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
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                                                                              /note-Torgan: colon; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I: Site_2: Eco RI: plasmid DNA from the normalized library NCI_CGAP_Colo was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1057416-1061255, and 114584-1145351).
                                         Subtraction by Bento Soares and M. Fatima Bonaldo. a 245 c 302 g 154 t 4 others
                                                                                                                                                                                                                                                        /clone="IMAGE:2389923"
/clone_lib="NCI_CGAP_Co16"
/tissue_type="colon tumor, RER+"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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CE 1 (bases 1 to 393)

RS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Firltchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.G., Liu, L.I., Marmaros, S.M., Merrick, J.M., Kelley, J.M., Kelley, J.C., Liu, L.I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nugyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Wedman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wel, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon
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EST177040 Jurkat T-cells VI Homo sapiens cDNA
similar to OX40 homolog, mRNA sequence.
AA306055
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Mammalia; Eutheria; Primates;
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Tel: 3018699056
Fax: 3018699423
                                                                                                                                                                                                             AW293499 arNA 471 bp mRNA UI-H-BIZ-ahg-a-02-0-UI.sl NCI_CGAP_Sub4 IMAGE:2727458 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          information related to this EST, please check Index (http://www.tigr.org/tdb/hgi/hgi.html) Seq primer: M13 Reverse.
Unpublished (1997)
Contact: Robert St
                              Tumor Gene Index
                                         Mammalia; Eutheria; Primates; Catarrhini; Hor
1 (bases 1 to 471)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Ana
                                                                                                                                                                            AW293499
AW293499.1 GI:6700135
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The Institute for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Venter,J.C.
Tritial assessment of human gene diversity and based upon 83 million nucleotides of cDNA sequentum 377 (6547 Suppl), 3-174 (1995)
                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: arkerlav@tigr.org
For clone availability,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Kerlavage,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Medical Center
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/db_xref="ATCC (inhost):160207"
/db_xref="taxon:9606"
/clone_lib="Jurkat T-cells VI"
/cell_type="T-lymphocyte"
/note="Vector: pBluescript SK-; S:Xhol"
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, Rockville,
                                                                                              Craniata; Vertebrata; Catarrhini; Hominidae
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                                              Project (CGAP),
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strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
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1456008-1456775, 1500552-1502855) NCI_CGAP_Kid5 pool 1:
LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE CloneIDs
1323912-1325831, 1471588-1472903, 1492104-1493255)
NCI_CGAP_Lu5 pool 1: LLAM 3575-3582, 3851-3854 (IMAGE CloneIDs 1414920-1417991, 1520904-1522439) NCI_CGAP_GC4
pool 1: LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE CloneIDs 1257096-1258631, 146906-1470983, 1475592-1476743
) NCI_CGAP_LD2 pool 1: LLAM 2457-2459, 2758-2759,
) NCI_CGAP_LD3 pool 1: LLAM 2457-2459, 2758-2759,
3062-3068 (IMAGE CloneIDs 98508-986759, 1101192-1101959,
1217928-1220615) NCI_CGAP_Col0 pool 1: LLAM 2644-2653,
2871-2872 (IMAGE CloneIDs 1057416-1061255, 1144584-1145351)
Subtraction was performed as previously described (Bonaldo, Lennon & Soares (1996): Normalization and Subtraction.
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145 c 1
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TAG_LIB=NCI_CGAP_Lei2
TAG_TISSUE=leiomyosarcoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/clone_lib="NCI_CGAP_Sub4"
/lab_host="DH10B (Life Technologies)"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC)
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Tissue Procurement: Life Technologies, Inc
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EST.
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Plate: LLAM11571 row: m column:
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                High quality sequence stop: 659.
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TAG_LIB-NCI_CGAP_Lei2
TAG_TISSUE-leiomyosarcoma
TAG_SEQ-AATCG"
TAG_SEQ-AATCG
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                                                                                 /organism-"Homo sapiens"
/db_xref-"taxon:9606"
                                                           /clone-"IMAGE:5227199"
                                                                                                                                           Location/Qualifiers
  /note="Organ:
                       /lab_host-"DH10B"
                                        /clone_lib-"NIH_MGC_120"
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                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11547-015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 198)
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Location/Qualifiers
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National Cancer Institute, Cancer Genome Anat
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a 275 c 235 g 98 t
/note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.25 kb. Life Technologies catalog #: 11547-015"

a 63 c 69 g 31 t 1 others
                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2850509"
/clone_lib="NCI_CGAP_Lym12"
                                                                                                      /lab_host="DH10B"
                                                                                                                                         /tissue_type="lymphoma,
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             Query Match
Best Local Similarity
Matches 142; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11449 row: k column: 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 172)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
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High quality sequence stop: 172.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
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ilarity 100.0%;
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                                                                                                     /note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NHH_MGC Library."
                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5180287"
/clone_lib="NHH_MGC_115"
                                                                                                                                                                                                                                                                                            /lab_host="DH10B"
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100.0%;
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Pred. No. 8.4e-7
                            Score 142; DB 10;
Pred. No. 3.8e-56;
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IMAGE:5180287 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 893)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (1999)
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High quality sequence stop: 593.
Location/Qualifiers
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Plate: LLAM11549 row: b column:
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/clone="IMAGE:5218473"
/clone_lib="NHF_MGC_118"
/tissue_type="leukocyte"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pCMV-SPORT6; Site_1: Not1; Site_2: ECORV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber
                                                                                                                                                                                                                                                                                                          (Invitrogen). Research Genetics this is a NIH_MGC Library." a 300 c 272 g 150 t
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mRNA sequence.
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Email: capabs-remail.nih.gov

This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through the This clone is available royalty-free through the This clone is available royalty-fr
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High quality sequence stop: 323.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/db_xref="taxon:9606"
/clone="IMAGE:2144971"
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                            sequence.
                                                                                                                                                                                                                                                                                                        op09h05.sl NCI_CGAP_Kid6 similar to SW:OX40_HUMAN
Unpublished (1997)
                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Ana
                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 398)
                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                AA970291.1 GI:3145804
EST.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11440 row: n column: 04
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Tissue Procurement: Life Technologies, Inc.
                        Tumor Gene Index
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone_11b="NIH_MGC_115"
/lab_host="DH10B"
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Pred. No. 1.3e-3
                                                                                                                                                                                                                                                                                                     398 bp mRNA linear EST 20-MAY-1998
Homo sapiens cDNA clone IMAGE:1575225 3'
P43489 OX40L RECEPTOR PRECURSOR ;, mRNA
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        cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortlum/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 373 Std Error: 0.00
Seq primer: -400P from Gibco.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 247)
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AI914208
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
seq primer: -00ml3 fwd. ET from Amersham
                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                            Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
/clone="IMAGE:1575225"
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/sex="mixed"
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Query Match
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IMAGE:2522697 3' similar to SV
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High quality sequence stop: 217.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/tissue_type="colonic mucosa from 3 patients with Crohn's disease"
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/clone="IMAGE:2337546"
/clone_lib="NCI_CGAP_Lu24"
                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2522697"
/clone_lib="Soares_Dieckgraefe_colon_NHCD"
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                                                                                                                  /lab_host="DH10B (phage-resistant)"
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0041 row: A column: 08
Seq primer: CGTTGTAAAACGACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
RMB. 308, Biomedical Polymers Resu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse whole genome plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 662)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZ320958 662 bp DNA linear GSS 29-SEP-200 1M0041A08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0041A08 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 662.
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Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
(http://www.jax.org/resources/documents/dnares/). The DNA
(http://www.jax.org/resources/documents/dnares/). The DNA
os hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
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                                                                                                                                                                                                  /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                  /organism-"Mus musculus"
/strain-"C57BL/6J"
/db_xref-"taxon:10090"
/clone-"UUGC1M0041A08"
/clone_lib-"Mouse 10kb plasmid UUGC1M library"
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                                                                                                                                                                                                                                                                                   /sex≂"Male"
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Best Local S
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630 bp mRNA linear EST 01-JUL-1997 vf97h05.rl Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:851769 5' similar to gb:Z21674 M.musculus Ox40 (MOUSE);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Marra M/Mouse EST Project
Washu-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuc
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 630)
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                                                                                                                                                                                                                                                                                                                                                                                                                                        MGI:503921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Waterston, R
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                                                           /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5'
                        /organism="Mus musculus'
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:851769"
                                                                                                                                                 /dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                            /tissue_type="mammary gland"
                                                                                                                                                                                                                   /sex="male"
                                                                                                                                                                                                                                       /clone_lib="Soares_mammary_gland_NbMMG"
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double-stranded cDNA was ligated to Eco RI s (Pharmacia), digested with Not I and cloned into
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1 (bases 1 to 342)

Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOllveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                         Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC6-NT0029-280
400-012-B08&t3=2000-04-28&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 342.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: +55-11-2707001
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llarity 100.0%;
Conservative (
2.0%; Silarity 100.0%; Conservative 0;
                                                                                                                  83
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                                                                                                          /note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone_lib="NT0029"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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Pred. No.
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                 DB 9;
43;
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1.8;
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 0;
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                                       Length 342;
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                                                                           RESULT :
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sequence.
AA312871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Colone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/Dbrp/Limagey.html
Insert Length: 811 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 437.
Location/Qualifiers
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AI823620.1 GI:5444291
                                AA312871 480 bp
EST183529 Jurkat T-cells VI Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
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National Cancer Institute, Cancer Genome Anat
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; plasmid DNA from the normalized library NCI_CGAP_Kid5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1323912-1325831, 1471368-1472903 and
                                                                                                                                                                                                                                                                                                                                                   Fatima Bonaldo.
94 c 18
                                                                                                                                                                                                                                                                                                                                                                              1492104-1493255). Subtraction by Bento Soares and Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:2398765"
/clone_lib="NCI_CGAP_Kid12"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                  mRNA linear E
sapiens cDNA 5' end,
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                                                                                                                                                                                                                                                                    Length 477;
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                                                        EST 19-APR-1997
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Matches 21
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                                                                                                                                                                                                                                                 237
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C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White
O., Sutton, G., Blake, J.A., Brandon, R.C., Gocayne, J.D., White
Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald
L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A.,
Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M.,
Kelley, J.C., Liu, L.-T., Marmaros, S.M., Merrick, J.M.,
Kelley, J.C., Liu, L.-T., Marmaros, S.M., Werrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W.,
Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L.,
Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon,
M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and
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                                                                                          482
qd77b04.x1 Soares_testis_NHT
3', mRNA sequence.
AI126122
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Email: arkerlavetigr.org
Email: arkerlavetigr.org
For clone availability, additional sequence and expression
Information related to this EST, please check the TIGR Human
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Eukaryota;
                   Homo sapiens
                                                                         AI126122.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Kerlavage, AR
                                        numan
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                                                                                                                                                                                                                                                                                                                                          Similarity
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/db_xref="ARCC (Inhost):160191"
/db_xref="taxon:9606"
/clone_lib="Jurkat T-cells VI"
/cell_type="T-lymphocyte"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pBluescript SK-;
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Pred. No.
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Ното
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44;
                                                                                                                               sapiens
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                                                                                                                               linear EST 28-OCT-1998 cDNA clone IMAGE:1735471
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688 tggggctgctgggccccctgg
                                        White,Y., Wylie,T., WashU-NCI human EST F
Unpublished (1997)
Contact: Wilson RK
Washington University School of 4444 Forest Park Parkway, Box
                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 545) Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Marti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consorttum/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 723 Std Error: 0.00
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1 (bases 1 to 482)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                 izman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., M., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., ite,Y., Wylie,T., Waterston,R. and Wilson,R.
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/db_xref="taxon:9606"
/clone="IMAGE:1735471"
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                                                                                                                                                                                                                                                                                                                                            Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
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1 (bases 1 to 572)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
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117 c 204 g 103 t 1 others
                                 /note-"Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6
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/db_xref="GDB:5940824"
/db_xref="taxon:9606"
/clone="IMAGE:740877"
 by Life Technologies
                    vector
                                                                                                                                            /clone="CSODC004YD06"
/clone_lib="LTI_NFL003_NBC3"
/sex="male"
                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                          /tissue_type="neuroblastoma cells"
/lab_host="DH10B"
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Contact : Feng Liang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dias Neto,E., Garcia Correa,R., Verjovski-Almelda,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOllveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Simpson, A.J. Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                                                                                                                      Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1-CM2&t2-CM2-CI0179-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: +55-11-2704922
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8371 Email: fliangelifetech.com URL:
http://fulllength.invitrogen.com"
a 134 c 191 g 86 t 27 othe
                                                                              /note-"Organ: colon_ins; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Technologies, a division of Invitrogen 9800 Medical Center
               tissue mRNA and cDNA amplification were performed under low stringency conditions."
189 c 173 g 131 t
                                                                                                                                                                                      /dev_stage="Adult"
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/db_xref="taxon:9606"
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Query Match Best Local Similarity

2.0%; 100.0%;

Score Pred.

21; No.

DB 45;

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Length 585;

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В

Locus

Michael

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RESULT 27
AI669655/c
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AI264358/c
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                                                        wc12a05.x1 |
similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the This Clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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636 bp mRNA linear EST 27-JAN-1999 q109f04.xl Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1855999 3' similar to TR:042154 042154 GLUCOSE-6-PHOSPHATASE;, mRNA
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                    A1669655
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EST.
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Location/Qualifiers
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_1: Eoc RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and scircles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ihAGE:1855999"
/clone_lib="Soares_NhHMPu_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pregnant uterus
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                                                      049 bp mRNA linear EST 17-DEC-1999 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2314928 3' TR:042154 042154 GLUCOSE-6-PHOSPHATASE;, mRNA sequence.
                                                                                                                                                                                                                                                                                                     2.0%;
                    GI:4834429
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Best Local :
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                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 650)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bbo.llnl.gov/Dbrp/image/image.html
Insert_Length: 768 Std Error: 0.00
                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue Procurement: Michael J. Brownstein, M.D., Ph Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                     mRNA sequence.
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cDNA Library Preparation: Ling Hong/Rubin Laboratory
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with a modified polylinker; Plasmid DNA from the
normalized library NCI_CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 110192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
a 154 c 230 g 117 t 7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:2314928"
/clone_lib="NCI_CGAP_pr28"
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No.
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sapiens cDNA clone
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IMAGE:5433602 5',
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BF7_25110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM1909 row: f column: 03
                                                                                                                                                                                                                                                                                                                                                                                                                    Wistow,G.J., Bernstein,S., Behal,A. and Smith,D. NEIBANK: EST analysis and bioinformatics for ocu Invest. Ophthalmol. Vis. Sci. 41 (2000) In press
                                                                                                                                                                                                         Email: graeme@helix.nih.gov
Plate: 12 row: c column: 11
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                          Contact: Wistow G Section on Molecular Structure and Function
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                                                                                                                                                                                                                                                                                              Tel: 301 402 3452 Fax: 301 496 0078
                                                                                                                                                                                                                                                                                                                                                         National Eye Institute
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/tissue_type="hepatocellular carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2: FOCRI; CDNA made by oligo-dT prining. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Library."
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/db_xref="taxon:9606"
/clone="IMAGE:5433602"
                     /tissue_type="Iris"
/dev_stage="Adult"
/lab_host="EMDH10B"
                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="bx12c11"
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                                                                                                        /clone_lib="Human Iris cDNA (Un-normalized, unamplified):
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://image.llnl.gov
Plate: LLCM1318 row: a column: 24
High quality sequence stop: 664.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      found through the I.M.A.G.E. Consortium/LLNL at:
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CDNA Library Arrayed by: The I.M.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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/clone_lib="NiH_MGC_14"
/tissue_type="renal cell adenocarcinoma"
/tissue_type="renal cell adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: kidney; Vector: pOTBP; Site_1: XhoI; Site_2:
/note="Organ: kidney; Vector: pOTBP; Site_1: XhoI; Site_2:
/note="Organ: kidney; Vector: pOTBP; Site_1: XhoI; Site_2:
/cloned into EccRI/XhoI sites using the following 5
/cloned into EccRI/XhoI sites using the following into Ec
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/db_xref="taxon:9606"
/clone="IMAGE:4587551"
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                                                                                                                                                                                                                             Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Compugen
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/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1981.DAT:*
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ACT-4; specific binding partner; sbd; B cells; lymphocyte; GVHD; graft versus host disease; immune response; transplantation; autoimmune disease; inflammation; HIV; human immunodeficiency virus; HTLV; human T lymphocyte virus; inflammatory bowel disease; screening; identification; ss.
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en OX-40 is specifically expressed on the cell surface of en activated T-cells, especially, for example, CD4+ T-cells. A CDNA encoding the human OX-40 homologue was cloned as follows the Experimental Autoimmune Encephalomyelitis model in rats X-40 antigen was identified (expressed on the surface of
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human cDNA Using the the OX-40

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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stimulatory primary signalling motif; immune cell; signal transduction; chimeric receptor; inflammatory disease; autoimmune disease; asthma; eczema; congenital disease; cystic fibrosis; sickle cell anemia; dermatological disease; psoriasis; neurological disease; multiple sclerosis; transplant-related disease; metabolic disease; organ transplant rejection; graft versus host disease; organ transplant rejection; graft versus host disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    270 G; 122 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 281;
                                                                                                                                                                                                                                                                                                                                                                                                                                          SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.6e-116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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RESULT
AAH24477
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Best Local
                                                                                                                                                                                                                                                                 Human; primary signalling motif; sequence block; SB; immunosuppressive secondary signalling sequence; antinicrobial; antifinflammatory; dermatological; neuroprotective; cytostatic; anti-HIV; antiasthmatic; antistokling; antipsoriatic; antidiabetic; gene therapy; diabetes; immune cell signal transduction; infection; inflammation; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       secondary signalling sequences. The specification describes stimulatory primary signalling motifs. Primary motifs are efficient at at mediating immune cell signal transduction, particularly when incorporated in an intracellular signalling domain of a chimeric receptor. The primary signalling motif can be combined in any way so as to achieve the desired level of activation (or inhibition) of a number of secondary messenger cascades. The signalling motifs are useful in therapy and in the manufacture of medicament for treating or preventing disease in humans or animals. They are are useful for treating lumman patients suffering from infectious diseases e.g. human fumunodeficiency virus (HIV) infections, inflammatory/autoimmune diseases such as asthma and eczema, congenital diseases e.g. cystic fibrosis, sickle cell anemia, dermatological diseases e.g. sporiasis, neurological diseases e.g. multiple sclerosis, transplant related disease e.g. organ
             Finney
                                                                                                                                                                                                                                     organ transplant
                                                                                                                                                                                                                                                                                                                                                                   Human
                                                                                                                                                                                                                                                                                                                                                                                                 07-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel cytoplasmic signalling protein and chimeric receptor protein, useful for treating HIV infection, asthma, eczema, psoriasis, multiple sclerosis, contain non-natural stimulatory primary signalling motif -
                                                                          01-NOV-1999;
                                                                                                          01-NOV-2000; 2000WO-GB04193
                                                                                                                                         10-MAY-2001
                                                                                                                                                                         WO200132867-A1
                                                                                                                                                                                                                                                   immune cell signal transduction; infect
autoimmune disease; congenital disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH24477 standard; DNA; 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oligonucleotides AAH24886-87 were used to construct DNA encoding
                                           (CELL-) CELLTECH CHIROSCIENCE
                                                                                                                                                                                                        Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transplant rejection, graft versus host disease, metabolic/idiopathic disease e.g. diabetes, and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acccccatccaagaggagcaggc 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cggagggaccagaggctgcccccgatgcccacaagccccctggggggaggcagtttccgg
                                                                                                                                                                                                       sapiens.
                                                                                                                                                                                                                                                                                                                                                               secondary signalling
             HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fig 3; 45pp; English.
             Lawson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B₽;
                                                                          99GB-0025853
                                                                                                                                                                                                                                      rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              c;
                                                                                                                                                                                                                                                                                                                                                                 motif SB34 oligo F1340A.
                                                                                                                                                                                                                                        SS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВP
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36
                                            GIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
2.3
                                                                                                                                                                                                                                                     psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                 immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC a consensus amino acid sequence. These motifs are extremely efficient at mediating immune cell signal transduction, particularly converted into an intracellular signalling domain of a chimeric receptor. Nucleic acids that encode, and polypeptides that contain, content of these primary signalling motifs are useful in medicine and research. They are useful in therapy, or in the manufacture of a medicament for treating or preventing disease in humans or in animals. These diseases cinclude infections (e.g. HTV (human immunodeficiency virus) infection), confine in the contain of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                          neurological disease; organ transplant rejection; diabetes; ca
graft-versus-host disease; adaptor receptor protein; sequence
SB; primary signalling motif; secondary signalling motif; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The
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                      01-NOV-2000; 2000WO-GB04189
                                                                 10-MAY-2001.
                                                                                                                                                                                                                                                            autoimmune disease; cystic fibrosis; sickle cell anaemia; psoriasis;
                                                                                                                                                                                                                                                                                  antisickling; antipsoriatic; neuroprotective; immunosuppressive;
antidiabetic; cytostatic; HIV infection; inflammation;
                                                                                                                                                                                                                                                                                                                              Human; anti-HIV; antiinflammatory; antiasthmatic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                       Human secondary signalling motif SB34 oligo F1340A.
                                                                                                                                                                                                                                                                                                                                                                                                                  08-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH24543 standard; DNA; 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cggagggaccagaggctgcccccgatgcccacaagccccctgggggaggcagtttccgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acccccatccaagaggagcaggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; 43pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to novel primary signalling motifs containing d sequence. These motifs are extremely
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36
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2.3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 117;
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RESULT 7 AAH24887/c

AAH24887;

22-AUG-2001

(first entry)

AAH24887 standard;

DNA;

117

dermatological disease; psoriasis; neurological disease; multiple sclerosis; transplant-related disease; metabolic disease; organ transplant rejection; graft versus host disease;

idiopathic

disease;

diabetes; cancer;

Stimulatory primary signalling motif; immune cell; signal transduction; chimeric receptor; inflammatory disease; autoimmune disease; asthma; eczema; congenital disease; cystic fibrosis; sickle cell anemia;

Oligonucleotide for a secondary signalling motif.

밁 Qy 멍 Š

66

acccccatccaagaggagcaggc

88 817

795

Query Match Best Local Matches

83;

Conservative

0

Similarity

100.0%; 7.8%;

Score 83; DB; Pred. No. 2.3
0; Mismatches

DB 22; .3e-27; 0,

Length 117;

0

Gaps

0,

65

735

cggagggaccagaggctgcccccgatgcccacaagccccctgggggaggcagtttccgg cggagggaccagaggctgccccccgatgcccacaagccccctgggggaggcagtttccgg

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CC receptor protein comprising an extracellular ligand-binding domain, a CC receptor protein comprising an extracellular signalling domain. The CC intracellular signalling domain and the comprises the cytoplasmic portion of at CC least one adaptor protein, and the extracellular ligand-binding domain in not CD8 or a major histocompatibility complex (MHC) class I protein. CC The adaptor receptor protein and the nucleic acid encoding it are useful in therapy. They are useful in the manufacture of a medicament for the CC treatment or prevention of disease in humans and animals. They are useful in the treatment of infectious diseases (e.g. HIV infection), CC congenital diseases (e.g. cystic fibrosis and sickle cell anaemia), CC congenital diseases (e.g. cystic fibrosis and sickle cell anaemia), CC dermatological diseases (e.g. psoriasis), neurological diseases (e.g. psoriasis), 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polynucleotide encoding adaptor receptor protein useful for treating human immunodeficiency virus (HIV) infection, asthma, cyfibrosis, multiple sclerosis, organ transplant rejection, diabete cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999;
Sequence 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CELL-) CELLTECH CHIROSCIENCE LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fig
  BP;
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  25
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Ą
45 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
36 G;
  11 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cystic
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RESULT 8
AAH24478/C
ID AAH244
XX AAH244
XX AAH244
XX O7-AUG
DT 07-AUG
DE Human
XX Human;
KW Second
KW Germat
KW dermat
KW antisi
KW antisi
KW antisi
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Best Local S
Matches 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mediating immune cell signal transduction, particularly when incorporated in an intracellular signalling domain of a chimeric receptor. The primary signalling motif can be combined in any way so as to achieve the desired level of activation (or inhibition) of a number of secondary messenger cascades. The signalling motifs are useful in therapy and in the manufacture of medicament for treating or preventing disease in humans or animals. They are are useful for treating human patients suffering from infectious diseases e.g. human immunodeficiency virus (HIV) infections, inflammatory/autoimmune diseases such as asthma and eczema, congenital diseases e.g. cystic fibrosis, sickle cell anemia, dermatological diseases e.g. psoriasis, neurological diseases e.g. multiple scierosis, transplant-related disease e.g. organ transplant rejection, graft versus host disease, metabolic/idiopathic
               antisickling; antipsoriatic; antidiabetic; gene therapy; diabetes;
immune cell signal transduction; infection; inflammation; cancer;
autoimmune disease; congenital disease; psoriasis; neurological di
                                                                 secondary signalling sequence; antimicrobial; anti-HIV; antiasthmatic;
dermatological; neuroprotective; cytostatic; anti-HIV; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                secondary signalling sequences. The specification describes stimulatory primary signalling motifs. Primary motifs are efficient at at mediating immune cell signal transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    scierosis,
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                                                                                                                                     Human secondary signalling motif SB34 oligo F1340B.
                                                                                                                                                                                                          AAH24478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel cytoplasmic signalling protein and chimeric receptor protein, useful for treating HIV infection, asthma, eczema, psoriasis, multi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CELL-) CELLTECH CHIROSCIENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                      Human;
                                                                                                                                                                                                                                            AAH24478
                                                                                                                                                                                                                                                                                                                                                             828
                                                                                                                                                                                                                                                                                                                                                                                                                            768
                                                                                                                                                                                                                                                                                                                                                                                            83
                                                                                                                                                                                                                                                                                                                             23
                                                                                                                                                                                                                                                                                                                                                                                          aagccccctgggggaggcagtttccggacccccatccaagaggagcaggccgacgccac
                                                                                                                                                                                                                                                                                                                                              tccaccctggccaagatc 845
                                                                                                                                                                                                                                                                                                                               TCCACCCTGGCCAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-389718/41
 transplant
                                                                                                      primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Conservative
                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treating HTV infection, asthma, eczema, psoriasis, multiple contain non-natural stimulatory primary signalling motif -
                                                                                                                                                                         (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP; 11 A;
                                                                                                      signalling motif; sequence block; SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99GB-0025848
   rejection;
                                                                                                                                                                                                                                          DNA;
                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35 C;
                                                                                                                                                                                                                                            117
                                                                                                                                                                                                                                                                                                                             σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer.
   88
                                                                                                                                                                                                                                            ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 78; DB red. No. 4e-0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22;
4e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 117;
                                                                                                      immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                   disease
                                                                                                                                                                                                                                                                                                                                                                                                                            827
                                                                                                                                                                                                                                                                                                                                                                                            24
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RESULT 9
AAH2454/C
ID AAH245
XX
AC AAH245
AC AAH245
XX
DT 08-AUG
DT 08-Human
XX
KW Human;

08-AUG-2001 AAH24544;

(first entry)

AAH24544 standard; DNA; 117

ВP

Human secondary

Human; anti-HIV; antiinflammatory; antiasthmatic; dermatological;

signalling motif SB34 oligo F1340B

밁 QΥ

Matches

78;

Conservative

0;

Mismatches

0;

Indels

0

Gaps

0;

4e-25;

Similarity

100.0%;

768 83

g Q

23

TCCACCCTGGCCAAGATC tccaccctggccaagatc 845

828

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The invention relates to novel primary signalling motifs containing CC a consensus amino acid sequence. These motifs are extremely cefficient at mediating immune cell signal transduction, particularly when incorporated into an intracellular signalling domain of a chimeric creceptor. Nucleic acids that encode, and polypeptides that contain, ct these primary signalling motifs are useful in medicine and research. They are useful in therapy, or in the manufacture of a medicament for contracting or preventing disease in humans or in animals. These diseases include infections (e.g. HIV (human immunodeficiency virus) infection), inflammatory or autoimmune diseases (e.g. asthma or eczema), congenital confidences (e.g. psoriasis), neurological diseases (e.g. psoriasis), neurological diseases (e.g. muttiple classes (e.g. psoriasis), neurological diseases (e.g. muttiple conserved to a large number of oligonucleotides used in the construction of sequence blocks (SBs) of primary and secondary constitution of the T cell receptor (TCR) complex. Secondary conserved in part secondary or constitution of the T cell receptor (TCR) complex. Secondary conserved in part secondary or constitution of sequence stimulatory or an inhibitory signal manual which regulates used in the tell support of the T cell receptor (TCR) complex. Secondary consolies in T cells.
Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acids encoding polypeptides with expanded primary signaling motifs, for use in gene therapy, particularly for treating or preventing infections, inflammations or autoimmune diseases in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                     Sequence 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Finney HM, Lawson ADG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-2000; 2000WO-GB04193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200132867-A1
                                                                                                            molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CELL-) CELLTECH CHIROSCIENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
                                                                                                          'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fig
                                                                                                            T cells.
                                                                       B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99GB-0025853
                                                                       11
                                                                     Α,
                                                                       <u>3</u>5
                                                                     Ç
Score 78;
Pred. No.
                                                                       45
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                                                                     <u>.</u>
               78;
                                                                       26
                                                                       T; 0 other;
               DB
               Length 117;
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RESULT 1
AAT00826
ID AATC
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                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                       inflammatory and autoimmune diseases (e.g. asthma and eczema), depending diseases (e.g. cystic fibrosis and sickle cell anaemia), dermatological diseases (e.g. psoriasis), neurological diseases (e.g.) multiple sclerosis) organ transplant rejection, graft-versus-host disease and metabolic/idiopathic diseases such as diabetes and cancer. The present sequence is one of a large number of oligonucleotides used in the construction of sequence blocks (SBs) of primary and secondary signalling motifs transduce either a stimulatory or an inhibitory signal, which regulates primary activation of the T cell receptor (TCR) complex. Secondary signalling motifs may be used as components of the adaptor receptor protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antisickling; antipsoriatic; neuroprotective; immunosuppressive; antidiabetic; cytostatic; HIV infection; inflammation; autoimmune disease; cystic fibrosis; sickle cell anaemia; psoria neurological disease; organ transplant rejection; diabetes; canc
                                                                                                                                                                                                                                                                                                                                                                                                                             is not CD8 or a major histocompatibility complex (MHC) class I protein. The adaptor receptor protein and the nucleic acid encoding it are useful in therapy. They are useful in the manufacture of a medicament for the treatment or prevention of disease in humans and animals. They are useful in the treatment of infectious diseases (e.g. HIV infection),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel nucleic acid encoding an adaptor a receptor protein comprising an extracellular ligand-binding domain, a transmembrane domain and an intracellular signalling domain. The intracellular signalling domain comprises the cytoplasmic portion of at least one adaptor protein, and the extracellular ligand-binding domain least one adaptor protein, and the extracellular ligand-binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polynucleotide encoding adaptor receptor protein useful for treating human immunodeficiency virus (HIV) infection, asthma, cynfibrosis, multiple sclerosis, organ transplant rejection, diabetee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           graft-versus-host disease; adaptor receptor protein; sequence block;
SB; primary signalling motif; secondary signalling motif; ss.
AAT00826 standard; cDNA to mRNA;
                                                                                                                                                                                                                                   Sequence 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Finney HM, Lawson ADG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CELL-) CELLTECH CHIROSCIENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-2000;
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                                                                                          828
                                                                 23
                                                                                                                  83 AAGCCCCCTGGGGGAGGCAGTTTCCGGACCCCCATCCAAGAGGAGCAGGCCGACGCCCAC
                                                                                                                                                                                Local
                            10
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                                                                                                                               aagccccctgggggaggcagtttccggacccccatccaagaggagcaggccgacgcccac 827
                                                                               tccaccctggccaagatc 845
                                                                 TCCACCCTGGCCAAGATC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-328790/34
                                                                                                                                                                     Similarity
78; Conser
                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                   BP; 11 A; 35 C; 45 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000WO-GB04189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99GB-0025854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52pp; English.
                                                                                                                                                                100.08; 1
                                                                                                                                                                               Score 78;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTD
                                                                                                                                                                    Mismatches
 618
                                                                                                                                                                                                                                   26 T; 0 other;
                                                                                                                                                                                DB 22;
4e-25;
                                                                                                                                                                     0
                                                                                                                                                                                           Length 117;
                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thma, cystic diabetes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               psoriasis;
                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer;
                                                                                                                                                                  Gaps
                                                                                                                  24
                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                      AAV32640
ID AAV3
                                                                                                                                                                                                                                                                                                                                                                                                                                                         멍
                                                                                                                                                                                                                                                                                                                                                               Q
                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 28
                                                                                       Key
CDS
                                                                                                                             Mus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baum PR,
 21-JUL-1998
                                                                                                                                                                                                                                               AAV32640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT00826;
                                                                                                                                                                                                                                                                                                                                        404
                                                                                                                                                                                                                                                                                                  11
                                                                                                                                                                                                                                                                                                                                                                                           28;
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glycoprotein cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated DNA encoding the OX40 ligand polypeptide and host cells, used to produce recombinant ligand used prim. T cell culture, to modulate immune response etc.
                                                                                                                                                         OX40; cytokine; T cell antigen; TH-2 immune response; OX40-L; OX40/Fc; ss.
                                                                                                                                                                                                                                                                                                           AAV32640 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5457035-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    membrane glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OX40; OX40-L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-1996
US5783665-A.
                                                                                                                                                                                                          Mouse OX40 extracellular domain encoding cDNA.
                                                                                                                                                                                                                                            25-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence encodes the extracellular domain of OX40, a membrane {
m glycoprotein} present on the CD4 positive subset of activated T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse type-II membrane polypeptide OX40 extracellular domain
                                                                                                                                                                                                                                                                                                                                                                                                          424 acaaccaggcctgcaagccctggaccaa 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                             acaaccaggcctgcaagccctggaccaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1995-357992/46
DB; AAR81881.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fanslow WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Column
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytokine; cell surface molecule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93US-0097827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93US-0097827
                            /*tag= a
/product= "Mouse OX40 extracellular region"
/note= "CDS does not contain a stop codon"
                                                                            Location/Qualifiers
1..618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-32; 26pp;
                                                                                                                                                                                                                                                                                                           cDNA to mRNA; 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Α;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gayle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 28; DB; Pred. No. 0.0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RВ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
                                                                                                                                                                                                                                                                                                                                                                                             431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goodwin
                                                                                                                                                                                                                                                                                                           ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 16;
0.0079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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RESULT 1
   S
                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents the mouse OX40 extracellular domain encoding cDNA. The extracellular domain of OX40 is its ligand binding domain. The present cDNA was used in the construction of the chimeric OX40/Fc cDNA (AAV32640). The invention claims for a murine OX40-L cytokine (AAW48975) that binds to the OX40 murine T cell antigen. The OX40-L protein is claimed to be useful for co-stimulation of T-cell production and in binding assays for detecting OX40 or its homologues. The OX40-L protein is also claimed to generate a TH-2
WPI; 1995-357992/46.
P-PSDB; AAR81882.
                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                              Baum
                                                                                   23-JUL-1993;
                                                                                                                        US5457035-A
                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                        0X40;
                                                                                                                                                                                                                         Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Col 31-32; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Purified polypeptide OX-40 ligands - production and binding assays for OX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JUL-1993;
22-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-JUN-1995;
                                              ( VMMI)
                                                                23-JUL-1993;
                                                                                                      10-OCT-1995
                                                                                                                                                                                                pDC406/0X40,
                                                                                                                                                                                                                                            30-MAR-1996
                                                                                                                                                                                                                                                             AAT00829;
                                                                                                                                                                                                                                                                              AAT00829 standard;
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                           404
                                                                                                                                                                                                                                                                                                                                    424 acaaccaggcctgcaagccctggaccaa 451
                                                                                                                                                                                                                                                                                                12
                                                                                                                                                                                                                                                                                                                          acaaccaggcctgcaagccctggaccaa 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1998-427099/36.
                                                                                                                                                                                             OX40-L; cytokine; cell surface molecule; 5/OX40/Fc*; membrane glycoprotein; ss.
                                              IMMUNEX CORP
                                                                                                                                                                                                                         pDC406/0X40/Fc*
                                                                                                                                                                                                                                                                                                                                                                       Similarity
                            Fanslow WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fanslow WC,
                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          вp;
                                                                                                                                                                                                                                           (first entry)
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95US-0494574
                                                                93US-0097827
                                                                                   93US-0097827
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                                                                                                                                                                                                                                                                                                                                                                                                          148
                                                                                                                                                   Location/Qualifiers
1..1317
                                                                                                                                                                                                                                                                              CDNA;
                                                                                                                                                                                                                                                                                                                                                                      2.6%;
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Y
                            Gayle
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                                                                                                                                          ø
                                                                                                                                                                                                                        encoding
                                                                                                                                                                                                                                                                                                                                                                                                          187
                                                                                                                                                                                                                                                                               1317
                                                                                                                                                                                                                                                                                                                                                                       .0%;
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                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                      Score
Pred.
                             RB,
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; for OX-40 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RВ,
                                                                                                                                                                                                                                                                               ВP
                                                                                                                                                                                                                                                                                                                                                                                                          151
                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goodwin
                             Goodwin RG;
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ი
                                                                                                                                                                                                                         OX40/Fc mutein
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Bd
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Best Local :
                                                                                                                                                                 This plasmid encodes an OX40/Fc antibody fragment mutein protein, and is used to express a soluble OX40/Fc mutein fusion protein for use in detecting cDNA clones encoding a OX40 ligand. The Fc fragment may be derived from human IgG1, and the plasmid may be used to transform the CV-1/EBNA (ATCC CRL 10478) monkey kidney cell line. Culture supernatant was purified by affinity chromatography and this was used, together with labeled goat anti-human IgG to
                                                                                                                                                                                                                                                                                                                        New isolated DNA encoding the OX40 ligand polypeptide and host cells, used to produce recombinant ligand used
                                                                                                                            Sequence 1317
                                                                                                                                                        screen various cell lines
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                                                                       Similarity
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                                                          Conservative
                                                                                                                            BP; 322 A; 417 C;
                                                                      2.6%;
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Pred. No.
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Chimeric -
                                          21-JUL-1998.
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                                                                                                                                                                                           mutation
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673..675
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mutant"
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l..1317
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fusion protein that contains the extracellular domain of mouse OX40 fused to the mutated Fc region of the human IgGl antibody. The fusion protein was used for detecting cDNA clones encoding an OX40 ligand. The invention claims for a murine OX40-L cytokine (AAW4897 that binds to the murine T cell antigen, OX40. The OX40-L protein is claimed to be useful for co-stimulation of T-cell production and in binding assays for detecting OX40 or its homologues. The OX40-L protein is also claimed to generate a TH-2 immune response.
                                                                                                                (WEIN/)
                             Nucleic acid encoding an activated T-cell antigen, Ox-40 - used develop prods. for detection and therapy of conditions mediated activated T-cells, eg. multiple sclerosis, rheumatoid arthritis,
                                                                        WPI;
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           Example;
                                                                                            Vandenbark AA,
                                                                                                                                              04-FEB-1994;
                                                                                                                                                                  06-FEB-1995;
                                                                                                                                                                                      10-AUG-1995
                                                                                                                                                                                                           W09521251-A
                                                                                                                                                                                                                              Synthetic
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                                                                                                                                                                                                                                                                                           21-DEC-1995
                                                                                                                                                                                                                                                                                                                                  AAQ93255 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1317 BP; 322 A; 417 C; 337 G;
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DB; AAW48976.
                                                                                                                WEINBERG A D.
CANTAB PHARM RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Col 35-38;
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llarity 100.0%;
Conservative
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          50;
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95US-0494574.
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                                                                                             Weinberg
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0.0074;
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RESULT 1
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Best Local S
Matches 24
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07-APR-2000;
30-JUN-2000;
01-SEP-2000;
                            The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences; and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and material form part of a set of probes for detecting the cytosine methylation and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antigen OX-40 is specifically expressed on the cell surface of antigen activated T-cells, especially, for example, CD4+ T-cells. A human cDNA encoding the human OX-40 homologue was cloned using primers 1 and 2. Template DNA for PCR amplification to product the human OX-40 cDNA can be extracted from the lambda GT11 cDNA library from human activated T-lymphocytes produced by Clontech, Palo Alto, California (Catalog No. HL10316).
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cancer; tumour; CpG dinucleoti
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24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of chemically modified genes associated with tumour suppressor oncogenes, useful in designing primers and probes for diseases associated with cytosine methylation state e.g.
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; 2000DE-1019173.
; 2000DE-1032529.
; 2000DE-1043826.
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genetic
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Best [
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                                                                                                                                                                                                                                                   01-NOV-1999;
13-APR-2000;
31-OCT-2000;
The present invention describes differentially expressed gene in anglogenesis (I), and the polypeptides that encode them. (cardiovascular activity, and can be used in the modulation of anglogenesis. The nucleic acids and polypeptides may be used prevention, diagnosis and treatment of diseases associated wi
                                                                                                                                                                                                                                                                                                                                                                                                                              Human; differentially expressed gene; anglogenesis; diagnosis; anglogenic disorder; wound healing; cancer; cardiovascular; psoriasis; vascular tumour; proliferative tumour; proliferative vitreoretinopathy; rheumatoid arthritis; Crohn's disease; atherosclerosis; endometriosis; neovascularisation; restenosis; hypertension; aneurysm; angina; myocardial infarction; chronic heart condition; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events whi are disadvantageous to patients. The present sequence is one of the 533 genomic sequences derived from tumour suppressor genes and
                                                                              Example
                                                                                                                   Differentially expressed genes involved in angiogenesis, useful treating e.g. vascular tumors, atherosclerosis and/or restenosis
                                                                                                                                                                                                                                                                                                       01-NOV-2000; 2000WO-US30051
                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
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                                                                                                                                                                                     Mehraban
                                                                                                                                                                                                                                                                                                                                 10-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                       PCR primer; hybridisation; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OX40 reverse
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                                                                                                    .g. vascular tumors, at
to balloon angioplasty
                                                                                                                                                                                                                                                   99US-0162699.
2000US-0196802.
2000US-0703350.
                                                                             Page 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                    Gerritsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR primer SEQ
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and modulate angiogenesis. The antibodies may also be used as diagnostic
agents for detecting the presence of the polypeptides in samples.

Disorders that may be prevented, diagnosed and/or treated by the above methods include, for example vascular tumours, proliferative tumours, attaining the province of the 
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Best Local S
Matches 22
                                                                                                                                                                                                 01-NOV-1999;
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Differentially expressed genes treating e.g. vascular tumors,
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vascular tumour; proliferative tumour; proliferative vitreoretinopa
rheumatoid arthritis; Crohn's disease; atherosclerosis; endometrios
neovascularisation; restenosis; hypertension; aneurysm; angina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inappropriate angiogenesis. The polypeptides may also be use in the production of antibodies against them and in assays to modulators of their expression and activity. The antibodies antagonists may also be used to down regulate expression and activity and the expression and activity.
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AAB98325 represent sequence used in
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Pred.
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  involved in angiogenesis, useful atherosclerosis and/or restenosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in assays to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            endometriosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    psoriasis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               identify
                    for
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subsequent to balloon angioplasty

182pp; English

present invention

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RESULT 1
AAA8760
ID AAA87
XX AAA6
AAC AAA6
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DT 04-L
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Matches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atherosclerosis, ovarian hyperstimulation, psoriasis, endometriosis associated with neovascularisation, restenosis subsequent to balloon angioplasty, scar tissue over production. peripheral vascular disease, hypertension, inflammatory vasculitides, Reynaud's disease and Reynaud's phenomenon, aneurysms, arterial restenosis, thrombophlebitis, lymphangitis, lymphedema, wound healing and tissue repair, ischaemia reperfusion injury, angina, myocardial infarctions, chronic heart conditions, heart failure such as congestive heart failure, age-related macular degeneration and osteoporosis. AAH22255 to AAH22325 and AAB98322 to AAB98325 represent sequence used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inappropriate angiogenesis. The polypeptides may also be used as antigens in the production of antibodies against them and in assays to identify modulators of their expression and activity. The antibodies and antipodies and antipodies and antipodies and activity and modulate angiogenesis. The antibodies may also be used to down regulate expression and activity and modulate angiogenesis. The antibodies may also be used as diagnostic agents for detecting the presence of the polypeptides in samples. Disorders that may be prevented, diagnosed and/or treated by the above methods include, for example vascular tumours, proliferative tumours, proliferative vitreoretinopathy, rheumatoid arthritis. Crohn's disease, the proliferative vitreoretinopathy, rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiinflammatory; cardiant; vulnerary; antiulcer; anticonvulsant;
antiparkinsonian; neuroprotective; antiviral; antibacterial; cytostatic;
antiparasitic; thrombolytic; anticoagulant; antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in angiogenesis (I), and the cardiovascular activity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein gene 15 SEQ ID NO:25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA87680 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer; immune system disorder; hyperproliferative disorder; infection;
cardiovascular disorder; neurological disease; wound healing;
                                                                                                  19-JAN-1999;
                                                                                                                                                               18-JAN-2000; 2000WO-US00903
                                                                                                                                                                                                                                                                                             WO200043495-A2
                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene therapy; vaccine; chemotaxis-modulator; angiogenesis-modulator;
                                 (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        955 ccaactctgcaccgttctagg 975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       secreted protein; immunosuppressive; immunostimulant; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first
                                                                                                  99US-0116330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                œ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; 4 G;
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Pred. No.
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14;
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Query Match Best Local S Matches 21

Similarity

100.0%; F

Mismatches NO.

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Gaps

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Score 21; Pred.

DB 10; 21;

Length 1153;

Conservative

Sequence 1153 BP;

241 A;

376 C;

279

ç;

255

T; 2

other,

RESULT 19 AAC76846

Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antiferantic; antihyroid; antibacterial; antifungal; antiferantic; antihyroid;

Human ORFX ORF2401 polynucleotide sequence SEQ ID NO:4801.

08-FEB-2001

(first entry)

AAC76846;

AAC76846 standard; cDNA; 1447 BP

antianaemic; gene therapy; cancer; prollferative disorder; hyperten neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; Ali cholesterol ester storage; systemic lupus erythematosus; infection;

hypertension

AIDS;

cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;

Homo sapiens thrombosis; damage;

contraceptive;

cartilage damage;

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antiarteriosclerotic and cytostatic. The secreted proteins and their polynucleotides can be used in gene therapy and as vaccines, chemotaxis-modulators and anglogenesis-modulators. The human secreted proteins and polynucleotides can be used for diagnosing (the susceptibility to) a pathological condition by determining the presence or absence of a mutation in the polynucleotide or determining the presence or amount of expression of the protein. The polynucleotides and proteins can also be used in the treatment and diagnosis of cancer,
                                                     diseases of the immune system, hyperproliferative disorders, cardiovascular disorders and neurological disease. They can also be used to promote wound healing and to fight infection. AAA87657 to AAA87665 are AAB25664 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                             immunostimulant; antiinflammatory; cardiant; vulnerary; antiulcer;
nootropic; antiviral; anticonvulsant; antiparkinsonian; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                 The polynucleotide sequences given in AAA87666 to AAA87708 encodes the human secreted proteins given in AAB25665 to AAB25755. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Examples of activities include: immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preventing, treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide encoding preventing, treating or ameliorating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosen CA, Rube
Komatsoulis G,
                                                                                                                                                                                                                                                                                                       antibacterial; antiparasitic; thrombolytic; anticoagulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ruben
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    451pp;
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CE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   secreted protein useful for medical condition -
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                                                                                                                                                            The polynucleotides and
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05-OCT-2000

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AAK52633
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AC AAK5
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W VACC
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                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   cc which represent the human OFFX open reading frames I to 316. The OFFX csequences have activities such as: cytostatic; hepatotropic; vulnerary; cc antiporiatic; anticonvulsant; antiarthritic; immunosuppressant; cc immunostinulant; cardiant; thrombolytic; coagulant; vasotropic; cc antidiabetic; hypotensive; dermatological; immunosuppressant; cc antidiabetic; hypotensive; dermatological; immunosuppressive; antiporiation; antibacterial; antiviral; antifungal; antirheumatic; cc antithyroid; and antianaemic. The sequences can be used for determining ct the presence of or predisposition to, or preventing or treating cc the presence of or predisposition to, or preventing or treating cc pathological conditions associated with an OFFX-associated disorder. The cnucleic acids can be used to express OFFX proteins in gene therapy cetors. The proteins and nucleic acids may be used to treat cancers, crolliferative disorders, neurodegenerative disorders, ostecarthritis, cf yraft vs host disease, cardiovascular disease, diabetes mellitus, thypertension, hypothyroidism, cholesterol ester storage, systemic lupus crythematosus, severe combined immunodeficiency (SCID), AIDS, viral, altoriman of ungal infection, malaria, autoimmune disorders, asthma, callergies, aplastic anaemia, burns, wounds, board artilage damage, coccurral haemoglobinuria, antiinflammatory disease; to enhance
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 21
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02-APR-1999;
05-APR-1999;
30-MAR-2000;
                 Homo
                                          Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                                       Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                     06-NOV-2001
                                                                                                                                                                                 AAK52633;
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                               AAK52633 standard;
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                                                                                                                     polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Page 3984-3985; 5507pp; English
                                                                                                                                                                                                                                                                                                                                                 Similarity 100
21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             1447
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99US-0127636.
99US-0127728.
2000US-0540763.
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Matches 21
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27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78333-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity in activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang
Zhao
                                                       Phosphatase; PP; immune disorder;
                                                                                                                                                                                                                                                                                                                                                  Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xue
                         Homo
                                             neuroprotective;
                                                                                           Human
                                                                                                                  17-SEP-2001
                                                                                                                                         AAH22958;
                                                                                                                                                               AAH22958
                                                                                                                                                                                                                                                                                                                            Sequence 1461
                                                                                                                                                                                                                                                                                                                                                                                                 treatment of
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                                                                                                                                                                                                                                688 tggggctgctgggccccctgg 708
                                                                                                                                                                                                                                                                                                                                                                                      inflammation
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)B; AAM79500.
                                                                                           phosphatase (PP) encoding
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                                                                                                                                                               standard;
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Wang D,
Yang Y,
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2000US-0560875.
2000US-0598075.
2000US-0623325.
2000US-0623325.
2000US-063561.
2000US-0693325.
2000US-0728422.
                                                                                                                                                                                                                                                                    Conservative
                                                                    PP;
                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                               cancer, leukaemia, nervous system disorders, arthritis and
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                                                                                                                                                                                                                                                                                                                             BP;
                                             Alzheimer's disease; Huntington's disease; human; cancer; nootropic; immunomodulatory; cytostatic; anticonvulsant; ss.
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Wang J,
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Wejhrman T,
                                                                                                                                                                                                                                                                                                                            249 A;
                                                                                                                                                               cDNA;
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                                                                                                                                                               1569
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Pred. No.
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10;
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F, C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang
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Location/Qualifiers

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Best Local
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28-JAN-2000;
25-FEB-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention provides human phosphatases (PP) and polynucleotides encoding the phosphatases. The polypeptides can be expressed by standard recombinant methodology. The PP are useful for treating a disease or condition associated with decreased expression of functional phosphatases. Compositions containing agonists or antagonists of PP may be used to treat a disease associated with decreased expression or overexpression of PP, respectively. Such diseases may include Alzheimer's disease, Huntington's disease, immune disorders, and cancers. The present sequence represents a human phosphatase encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel phosphatases useful for treating diseases associated with decreased expression of functional phosphatases, e.g., Alzheimer's disease, Huntington's disease, immune disorders, and cancers -
                                                                                                                                                 vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                Human; cytokine;
                                                                                                                                                                                                                                                        Human polynucleotide SEQ ID NO
                                                                                                                                                                                                                                                                                                     06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                        AAK51649
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                                                                                                                                               system
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nilarity 100.0%;
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g E,
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                                                                                                                                                                                                                cell proliferation; cell differentiation;
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                                                                                                                                                                                                                                                                                                     entry)
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                                                                Homo sapiens.
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RESULT 23
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ID AAL360
XX
AAC AAL360
XX
DT 08-JAN
DT UMBAN
DE Human
XX
Cytost
KW Cytost
KW antial
KW vulner
KW reardia
KW reardia
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Best Local S
Matches 21
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27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
30-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                       1178
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Zhao
                                                                                         Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
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                                                                   cardiant; gene therapy; cancer; immune neurological disease; infection; human;
                                                                                                                                         Human
                                                                                                                                                                08-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                             Sequence 1658
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DB; AAM78516.
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Wang D,
Yang Y,
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, Wang J, Zh
Wejhrman T,
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Zhang J, Ren
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31-JAN-2000
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24-FEB-2000
116-MAR-2000
117-MAR-2000
117-JUL-2000
117-JUL-
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  2000US-0179065.
2000US-0188608.
2000US-0188661.
2000US-0188674.
2000US-0188674.
2000US-0198123.
2000US-0198123.
2000US-0198135.
2000US-0116846.
2000US-0116846.
2000US-02116880.
2000US-0211689.
2000US-02118290.
2000US-02118290.
2000US-0215213.
2000US-0215214.
2000US-0225214.
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2000US-0225214.
2000US-0225277.
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2000US-0225277.
2000US-0225777.
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    29-SEP 2000
29-SEP 2000
20-CCT 2000
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03-CCT 2000
03-CCT
    WPI;
                                          Rosen
2001-451937/48
                                          CA,
                                        Barash
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2000US - 0236379
2000US - 0236370
2000US - 0236370
2000US - 0237039
2000US - 0237039
2000US - 0241785
2000US - 0241787
2000US - 0241808
2000US - 0246474
2000US - 0246474
2000US - 0246477
2000US - 0246673
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2000US - 0246611
2000US - 0249211
2000US - 0249216
2000US - 0249219
2000US - 0251189
2000US - 0251189
2000US - 0251189
2000US - 0251989
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RRESULT 2
AAK6970
ID AAKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to novel genes (AAL34669-AAL37666) and proteins C (ABB03087-ABB04109) associated with the musculoskeletal system useful CC for preventing, treating or ameliorating medical conditions e.g. by CC protein or gene therapy. The genes are isolated from a range of human C tissues disclosed in the specification. The nucleic acids, proteins, CC antibodies and (antiagonists are useful in the diagnosis, treatment CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and CC other cancers of the adrenal gland, bone, bone marrow, breast, CC gastrointestinal tract, liver, lung, or urogenital; (b) immune CC disorders e.g. Addison's disease, allergies, autoimmune hemolytic CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; CC (c) cardiovascular disorders such as myocardial ischaemias; (d) wound CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and of the fortions diseases such as viral, bacterial, fungal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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04-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic;
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parasitic infections.

Note: The sequence data for this patent did not form part of Note: The sequence data for this patent did not form part of Note: The sequence data for this patent did not form part of Note: The sequence data for this patent did not form part of Note: The sequence data for this patent did not form part of Note: The sequence data for this patent did not form part of Note: The sequence data for this patent did not form part of Note: The sequence data for this patent did not form part of Note: The sequence data for this patent did not form part of Note: The sequence data for this patent did not form part of Note: The sequence data for this patent did not form part of Note: The sequence data for this patent did not form part of Note: The sequence data for this patent did not form part of Note: The sequence data for this patent did not form part of Note: The sequence data for this patent did not form part of Note: The sequence data for this patent did not form part of Note: The sequence data for this patent did not form part of Note: The sequence data for this patent data for this patent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human;
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WIPO at ftp.wipo.int/pub/r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immune; haematopoietic; immune/haematopoietic antigen; cancer;
atic; gene therapy; vaccine; metastasis; ds.
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    2000US-0179065.

2000US-0180628.

2000US-0184664.

2000US-0186350.

2000US-018974.

2000US-0198123.

2000US-0198123.

2000US-0205515.

2000US-020467.

2000US-0214886.

2000US-0214886.

2000US-0216647.
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    14-SEP 2000;
21-SEP 2000;
21-SEP 2000;
25-SEP 2000;
26-SEP 2000;
27-SEP 2000;
27-SEP 2000;
29-SEP 2000;
20-OCT 2000;
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08-SEP-2000;
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05-SEP-2000;
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22-AUG-2000;
22-AUG-2000;
23-AUG-2000;
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14-SEP-2000;
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06-SEP-2000;
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2000US-0232081.
2000US-0231968.
2000US-0232397.
2000US-0232398.
2000US-0232399.
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2000US-0229509.

2000US-0229513.

2000US-0230437.

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2000US-0231243.

2000US-0231243.

2000US-0231244.

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2000US-0231413.
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2000US-0217487
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2000US-0224518
2000US-0225213
2000US-0225213
2000US-0225214
2000US-0225214
2000US-0225266
2000US-0225266
2000US-0225267
2000US-0225267
2000US-0225268
2000US-0225775
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2000US-02257759
2000US-0225779
2000US-0239935.
2000US-0239937.
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2000US-0234223.
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2000US-0232401.
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2000US-0237040.
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2000US-0235834
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2000US-0236327.
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis an treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a pattient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I)
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01-NOV-2000

08-NOV-2000

17-NOV-2000

17-NO
                                                                                                                                                                                                      Disclosure;
                                                                                                                                                                                                                                         Nucleic acids encoding useful for preventing, metastasis -
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                                                                                                                                                                                                                                                                                                                        2001-483426/52.
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2000US-0254097.
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2000US-0251869
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2000US-0241826.
2000US-0244617.
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diagnosing
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osing and/or treating
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and

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RESULT 2
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       14 - JUL - 2000
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19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
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11-JUL-2000;
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoletic-related diseases, especially cancers and cancer metastases of haematopoletic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoletic antigen genomic sequences from the present invention. AAK84942 to AAK84950 and AAM82169
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       2000US-0189874

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2000US-0214886

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2000US-0217486

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer;
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2000US-0229509 2000US-0229513 2000US-0230437 2000US-0230438 2000US-0231243 2000US-0231243 2000US-0231244 2000US-0231413 2000US-0231414 2000US-0231414

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                             Ωy
                                                                                                                                    CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic continity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and ctreatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome cc that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting CC the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent. CC diagnose and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic antigen genomic CC sequences from the present invention. AAK54950 and AAM82169 CC represent sequences used in the exemplification of the present invention.
                                                         Query Match 2.0
Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
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17-NOV-2000
01-DEC-2000
05-DEC-2000
05-DEC-2000
05-DEC-2000
05-DEC-2000
06-DEC-2000
   34516
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO
                                                                                                                                    Sequence 38348 BP;
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                               684
gtgctggggctgctgggcccc 34536
              gtgctggggctgctgggcccc
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                                                                                                                                                                sequences used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barash SC,
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2000US-0249210

2000US-0249211

2000US-0249211

2000US-0249213

2000US-0249214

2000US-0249216

2000US-0249216

2000US-0249216

2000US-0249217

2000US-0249244

2000US-0249245

2000US-0249265

2000US-0249265

2000US-0249265

2000US-0249297

2000US-0249297

2000US-0250160

2000US-0250160

2000US-0251179

2000US-02511856

2000US-02511856

2000US-02511858

2000US-02511858
                                                                                                                                   9411 A; 7405 C; 8303 G;
                                                                         2.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     39765; 3071pp + Sequence Listing; English.
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                             704
                                                            0;
                                                                          Score 21;
Pred. No.
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                                                            Mismatches
                                                                                                                                                                exemplification
                                                                          DB 22;
7.5;
                                                                                                                                    13229
                                                            0;
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                                                                                       Length 38348;
                                                                                                                                    Τ,
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                                                                                                                                                                the present invention
                                                                                                                                    0 other;
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                                                           Gaps
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and

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22-AUG-2000
22-AUG-2000
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23-AUG-2000
23-AUG-2000
21-SEP-2000
01-SEP-2000
01-SEP-2000
01-SEP-2000
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01-SEP-2000
02-OCT-2000
03-NOV-2000
03-NOV-2000
03-NOV-2000
08-NOV-2000

2000US-0232081
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2000US-0232398
2000US-0232399
2000US-0232401
2000US-0233063
2000US-0233063
2000US-0234274
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2000US-0237037

2000US-0241808 2000US-0241809 2000US-0244617 2000US-0246474 2000US-0246476 2000US-0246476 2000US-0246476 2000US-0246477 2000US-0246477 2000US-0246523 2000US-0246523 2000US-0246524 2000US-0246526 2000US-0246526 2000US-0246527 2000US-0246527 2000US-0246528 2000US-0246528 2000US-0246528 2000US-0246528 2000US-0246610 2000US-0246610 2000US-0246611 2000US-0246611

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RESULT 2
ABL15756
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AC ABL1
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ABL17164
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                                                                                                                                                                                    Query Match
Best Local S
Matches 20
                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
  'Drosophila;
                       Drosophila
                                                                                                                                                                                                                                                           The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                            26-MAR-2002
                                                                                      ABL15756 standard;
                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 2965; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-656860/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide;
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                                                                 ABL15756;
                                                                                                                                                                                                                                         Sequence 4466 BP; 1312 A; 945 C; 916 G; 1293 T;
                                                                                                                                                                                                                                                                                                                                                                                                               interactions
                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PEKE ) PE
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster genomic polynucleotide SEQ ID NO 2965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL17164 standard;
                                                                                                                                                               994
                                                                                                                                           186
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les 20; Conser
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                                                                                                                                         gctctctgcttacgtatgcc
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                      melanogaster expressed
 developmental biology; cell signalling; insecticide;
                                                                                                                                                                                    1.9%; Sillarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-191637P.
2000US-0614150.
                                          (first entry)
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                                                                                      cDNA; 6361 BP
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                                                                                                                                           205
                                                                                                                                                                                                                                                                                                                                                                                                                         detection reagent for detecting for elucidating cell signalling
                                                                                                                                                                                              Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Myers
                                                                                                                                                                                    Mismatches
                      polynucleotide
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25;
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                                                                                                                                                                                                        Length 4466;
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and cell-cell
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AAK84952
ID AAK8
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Best Local S
Matches 20
                                                                                                                                                                                                                                                                                                                               5437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL116176-ABL30511), expressed DNA sequences (ABL116176-ABL30511) sepressed DNA (ABB57737-ABB72072).
31-JAN-2000;
04-FEB-2000;
                                                                                                                                                                                                            07-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-656860/75.
P-PSDB; ABB71653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pharmaceutical; gene;
                                    17-JAN-2001; 2001WO-US01354
                                                              09-AUG-2001
                                                                                       WO200157182-A2
                                                                                                                                           cytostatic;
                                                                                                                                                                                 Human immune/haematopoietic antigen genomic sequence
                                                                                                                                                                                                                                      AAK84952;
                                                                                                                                                                                                                                                              AAK84952 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6361 BP; 1759 A; 1273 C; 1395 G; 1934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence data for this patent did not form specification, but was obtained in electronic i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 41750; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genes from Drosophila
interactions •
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                  Conservative
2000US-0179065
2000US-0180628
                                                                                                                                                                                                            (first
                                                                                                                                                       haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                           therapy; vaccine;
                                                                                                                                                                                                                                                              DNA; 38272
                                                                                                                                                                                                           entry)
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                            metastasis;
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2000US-0218290.
2000US-022963.
2000US-022964.
2000US-0225266.
2000US-0225266.
2000US-0225268.
2000US-0225759.
2000US-0225759.
2000US-0225759.
2000US-0225759.
2000US-0225759.
2000US-0225768.
2000US-0225759.
2000US-0225759.
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2000US-02258681.
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2000US-023124.
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2000US-0234299.
2000US-0234299.
2000US-0235834.
2000US-0236367.
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2000US-0186350

2000US-0189874

2000US-0199076

2000US-019025

2000US-0205515

2000US-0209467

2000US-0214886

2000US-0214647

2000US-0216647

2000US-0217487

2000US-0217487

2000US-0217487
   02-OCT-2000
02-OCT-2000
13-OCT-2000
21-OCT-2000
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26-NOV-2000
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28-NOV-2000
28-NOV-2000
29-OCT-2000
20-OCT-2000
20-NOV-2000
20-OCT-2000
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20-NOV-2000
20-OCT-2000
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20-NOV-2000
20-OCT-2000
20-NOV-2000
21-NOV-2000
21-NOV
                              Nucleic acids encoding useful for preventing, metastasis -
                                                                                                                        Rosen
 Disclosure; SEQ
                                                                                                                                                      ( HUMA - )
                                                                                                                      CA,
                                                                                                                                                      HUMAN GENOME
                                                                                                                        Barash
                                                                                                                                                                                 2000US-0237039.
2000US-0237040.
2000US-0239937.
2000US-02440960.
2000US-0241785.
2000US-0241808.
2000US-0241808.
2000US-0244617.
2000US-0246477.
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2000US-0246523.
2000US-0246523.
2000US-0246611.
2000US-0246611.
2000US-0246611.
2000US-0246611.
2000US-0249217.
2000US-0249218.
2000US-0249218.
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2000US-0249218.
2000US-0249218.
2000US-02511868.
2000US-0251988.
2000US-0251988.
2000US-0251989.
2000US-0251989.
ID NO 39764; 3071pp + Sequence Listing; English
                                                                                                                        SC,
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                                            human immur
diagnosing
                                                                                                                         Ruben
                                            immune/hematopoietic osing and/or treating
                                                                                                                         SM
                                            antigen polypeptides, cancers and
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24 FEB-2000 16-MAR-2000 16-MAR-2000 11-MAR-2000 11-MAR-2000 20-JUN-2000 20-JUN-2000 20-JUN-2000 20-JUN-2000 20-JUN-2000 21-JUL-2000 22-JUL-2000 23-JUL-2000 24-JUL-2000 25-SEP-2000 20-SEP-2000 21-SEP-2000 22-SEP-2000 23-SEP-2000 24-SEP-2000 25-SEP-2000 29-SEP-2000 20-CCT-2000 20-CCT-2000 20-CCT-2000 20-CCT-2000

Example 19; Page 147; 182pp; English

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13-APR-2000;
31-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAK54951 to AAK64702 encode the human immune/haematopoletic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polyuncleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polyuncleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoletic-related diseases, especially
                                                                                                                                                                                                                                                                                                                                                                                                                          Human; differentially expressed gene; anglogenesis; diagnosis; anglogenic disorder; wound healing; cancer; cardiovascular; psoriasis; vascular tumour; proliferative tumour; proliferative vitreoretinopathy; rheumatoid arthritis; Crohn's disease; atherosclerosis; endometriosis; neovascularisation; restenosis; hypertension; aneurysm; angina; myocardial infarction; chronic heart condition; osteoporosis;
               subsequent
                                                                                                                                                                                                                                                               01-NOV-2000; 2000WQ-US30051
                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OX40 hybridisation probe SEQ ID NO:20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH22274;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169
                                treating
                                              Differentially expressed
                                                                                WPI; 2001-291056/30
                                                                                                                                                                                                                                                                                               10-MAY-2001
                                                                                                                                                                                                                                                                                                                                WO200132926-A2
                                                                                                                                                                                                                                                                                                                                                                                                             PCR primer; hybridisation; probe;
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                                                                                                               Mehraban
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                 GENENTECH INC
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               to balloon angioplasty
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2000US-0196802.
2000US-0703350.
                                                                                                                 Gerritsen
                           expressed genes involved in anglogenesis, useful for vascular tumors, atherosclerosis and/or restenosis
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antagonists may also be used to down regulate expression and activity and modulate angiogenesis. The antibodies may also be used as diagnostic agents for detecting the presence of the polypeptides in samples. Sisorders that may be prevented, diagnosed and/or treated by the above methods include, for example vascular tumours, proliferative tumours, proliferative tumours, crohn's disease, atherosclerosis, ovarian hyperstimulation, psoriasis, endometriosis associated with neovascularisation, restenosis subsequent to balloon angioplasty, scar tissue over production, peripheral vascular disease, hypertension, inflammatory vasculitides, Reynaud's disease and Reynaud's phenomenon, aneurysms, arterial restenosis, thrombophlebitis, lymphedema, wound healing and tissue repair, ischaemia creperfusions injury, angina, myocardial infarctions, chronic heart conditions, heart failure such as congestive heart failure, age-related macular degeneration and osteoporosis. AAH22255 to AAH22325 and AAB98322 crepresent sequence used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inappropriate angiogenesis. The polypeptides may also be used as antigens in the production of antibodies against them and in assays to identify modulators of their expression and activity. The antibodies and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes differentially expressed genes involved in angiogenesis (I), and the polypeptides that encode them. (I) have cardiovascular activity, and can be used in the modulation of angiogenesis. The nucleic acids and polypeptides may be used in the prevention, diagnosis and treatment of diseases associated with
                                                     present invention.
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                                                                                                             WO200155314-A2
                                                                                                                                       digestive system
                                                                                                                                                                   Human
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                                                                                                                                                                                             AAK87821;
                                                                                                                                                                                                          AAK87821 standard; cDNA;
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                                                                                                                                                                 digestive
                                                                                                                                                                               (first entry)
                                                                                  2001WO-US01324
                                                                                                                                                                 system antigen coding sequence SEQ ID NO: 137
                                                                                                                                        disorder; Meckel's
                                                                                                                                                                                                           637
                                                                                                                                                                                                           ВP
                                                                                                                                             n; gene therapy; cancer;
Hirschsprung's disease;
                                                                                                                                              appendicitis;
chronic colit
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colitis;

31-JAN-2000; 04-FEB-2000; 24-FEB-2000; 02-MAR-2000; 16-MAR-2000; 17-MAR-2000; 18-APR-2000; 19-MAY-2000; 07-JUN-2000;

2000US-0179065 2000US-0180628 2000US-0184664 2000US-0188350 2000US-0189874 2000US-0199123 2000US-0199123 2000US-0205515 2000US-0205467 2000US-0215135

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             The present invention provides the protein and coding sequences number of human digestive system antigens. These can be used in diagnosis, treatment and prevention of digestive system disorder including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic coliticularies and the present sequence is a cDNA encoding a discretive colitis. The present sequence is a cDNA encoding a discretive colitis.
                                                                                                                                                                           Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders digestive system, particularly cancer and cancer metastases.
                                                                                                                                           Claim
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P-PSDB; AAM92048.
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2000US-0241786

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Source 637 BP, 142 A: 193 C: 147 G: 150 T: 5 other:

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 362 typicoticotygeoctygy 380

Search completed: June 19, 2002, 02:21:30

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US-08-098-4794-574-10
US-08-192-480A-2
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Sequence 15, App		Sequence 1, Appl	1,	Sequence 4, Appli	26	Sequence 2, Appl:	Sequence 3, Appl	Sequence 3, Appl	Sequence 3, Appl	Sequence 3, Appl	Sequence 3, Appl.	2,	Sequence 9, Appl	•	Sequence 2, Appl	Sequence 3, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 5, Appl	Sequence 5, Appl:	Sequence 26, App	Sequence 270, App
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## Sequence 1. Application US/08147784 Patent No. 5821332 GENERAL INFORMATION: GAPPLICANT: Bodfrey, Wayne APPLICANT: Bodfrey, Wayne APPLICANTON: CD4+ T-CELLS: ACT-4 NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: ADDRESSE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue CITY: Palo Alto STATE: Callifornia COUNTRY: US ZIP: 94301 COMPUTER: Bod Alto STATE: Callifornia COUNTRY: BOD COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION NUMBER: US/08/147,784 FILING DATE: 03-NOV-1993 CLASSIFICATION NUMBER: 30,223 REFERENCE/DOCKET NUMBER: 30,223 REFERENCE/DOCKET NUMBER: 30,220 TELEFAX: (415) 326-2420 INFORMATION FOR SED ID NO: 1: SEQUENCE CHARACTERISTICS: LEGGTH: 1057 base pairs TYPE: nuclei acid

; OTHER INFORMATION: US-08-147-784-1

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LOCATION: 15.845
COTHER INFORMATION: US-08-195-967-1
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NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 0549
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08195967 Patent No. 6242566 GENERAL INFORMATION:
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Best Local Similarity
Matches 1056; Conserv
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/195,967
FILING DATE: 10-FEB-194
CLASSIFICATION: 424
CLASSIFICATION: 424
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APPLICANT: Engleman, Edgar G.
TITLE OF INVENTION: LIGAND (ACT-4-L) TO
TITLE OF INVENTION: CD4+ T-CELLS
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Sequence 1, Application US/08472940
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                                                       GENERAL INFORMATION:
            APPLICANT: Godfrey, Wayne
APPLICANT: Buck, David
APPLICANT: Engleman, Edgar G.
TITLE OF INVENTION: RECEPTOR ON THE SURFACE
TITLE OF INVENTION: CD4+ T-CELLS: ACT-4
NUMBER OF SEQUENCES: 2
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      CORRESPONDENCE
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NAME: Smith, Willaim M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 0549
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 1056; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/
FILING DATE: 03-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Willalm M
REGISTRATION NUMBER: 30,22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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CITY: Pa
STATE: C
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: 15..845
OTHER INFORMATION:
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Palo Alto
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US-08-192-480A-1
; Sequence 1, Application US/08192480A
; Patent No. 5759546
; GENERAL INFORMATION:
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APPLICATION NUMBER: US
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: MS DOS SOTTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA:
                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1021
                                                                                                                                                                                                                                                        TITLE OF INVENTION: TREATMENT OF CD4 T-C
TITLE OF INVENTION: MEDIATED CONDITIONS
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                      APPLICANT: Andrew D. Weinberg and Arthur A. APPLICANT: Vandenbark
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106
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                                                                                                                                                                              ADDRESSEE: Richard J. Polley, Esq.
ADDRESSEE: Klarquist Sparkman Campbell
ADDRESSEE: Leigh & Whinston
STREET: 121 S.W. Salmon Street, Suite 1600
CITY: Portland
STATE: Oregon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    960
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                                                                                                                                                                  COUNTRY:
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                                                                                                                                                    E: Oregon
TRY: United States
97204
                                                                                                                          Disk, 3-1/2 inch
                                                                                                                                                                                                                                                                                                         TREATMENT OF CD4 T-CELL
                                                        US/08/192,480A
                                                                                                                                                                  of America
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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Richard J. Polley, Esq.
REGISTRATION NUMBER: 28,107
REFERENCE/DOCKET NUMBER: 4282-3;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 226-7391
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 848 base pairs
TYPE: Nucleic acid
STRANDEDNESS: DOUBLE
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
US-08-097-827-6
; Sequence 6, Application US/08097827
; GENERAL INFORMATION:
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HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243
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                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
FILING DATE: 23-ULI-1993
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Novel Cytokine Which
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Baum, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      agccgctcccagaacacggtgtgccgtccgtgcgggccgggcttctacaacgacgtggtc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 98101
                                                                                                                                                                                                                                                                                                                  Goodwin, Ray
Fanslow, William
Gayle, Richard
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                                                                   Version
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                                                                   #1.25
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. LOCATION: 1..618; SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-08-097-827-6
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                        COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,574
FILING DATE: 22-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNUMBER: US/08/097,827
FILING DATE: 23-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2806
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                    TELEPHONE: 206-587-073
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 206-58 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Goodwin, Ray
APPLICANT: Fanslow, William
APPLICANT: Gayle, William
APPLICANT: Gayle, No. 5783665el Cytokine Which is a Ligand for
TITLE OF INVENTION: 0X40
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: cDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2806
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: MOUSE OX40
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No. 5783665
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                                                                                                                                                                                                                                                                                                                                                                                                                   Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 618 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                    WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08494574
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LOCATION: 1...
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ilarity 100.0%;
Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunex Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206-587-0730
                      6:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
0.0015;
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; LOCATION:
US-08-494-574-6
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SEQUENCE DESCRIPTION: SEQ ID NO: 10: US-08-097-827-10
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                                                                                                                                                                                                                                                                       TELEPHONE: 206-587-0 INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
FILING DATE: 23-Jul-1993
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
                                                                                                      TOPOLOGY: linear MOLECULE TYPE: CNA HYPOTHETICAL: NO ANTI-SENSE: NO IMMEDIATE SOURCE:
                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                        FEATURE:
                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 206-587-0730
                                   NAME/KEY:
LOCATION:
                                                                                    CLONE: MOX40Fc Mutein
                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                 TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Immunex Corporation STREET: 51 University Street
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CDS

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Sequence 10, Applicati
GENERAL INFORMATION:
APPLICANT: Baum
                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                  HYPUIGE NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:

TONE: MOUSE 0X40
                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: LINEAL MOLECULE TYPE: CDN
                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE N
HYPOTHETICAL: NO
                                                                                                                                                                                                      424 acaaccaggcctgcaagccctggaccaa 451
                                                                                                                                                                                      404 ACAACCAGGCCTGCAAGCCCTGGACCAA 431
                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                     TITLE OF INVENTION: Novel Cytokine Which is a Ligand for
                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
                                                                                                                     Application US/08097827
                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                       1..618
                                                  Goodwin, Ray
Fanslow, William
Gayle, Richard
                                                                                            Baum, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                        2.6%; Score 28;
100.0%; Pred. No.
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                                                                                                                                                                                                                                                        DB 1;
. 0.0015;
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US-08-494-574-10
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                                                              Query Match
Best Local Similarity
Matches 28; Conserv
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                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPDIOCEY: 110er
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                      TOPOLOGY: 1110ca.
MOLECULE TYPE: CDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,574
FILING DATE: 22-JUN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 206-587-0730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Fanslow, William
APPLICANT: Gayle, Richard
TITLE OF INVENTION: No. 5783665el Cytokine Which is a Ligand for
TITLE OF INVENTION: OX40
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                            HYPOTHETICAL:
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 23-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                             IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
 404
                  424 acaaccaggcctgcaagccctggaccaa 451
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                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Perkins, Patricia A. REGISTRATION NUMBER: 34,69 REFERENCE/DOCKET NUMBER: 2
                                                                                                                                                                                                              CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 2.6%; So
Local Similarity 100.0%; I
nes 28; Conservative 0;
                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/097,827
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ACAACCAGGCCTGCAAGCCCTGGACCAA 431
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51 University Street
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                                                            2.6%; So llarity 100.0%; I Conservative 0;
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                                                                                                                                                                                                                                                                                           linear
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                                                                             Score 28;
Pred. No.
                                                              Mismatches
                                                                             DB 1;
0.0014;
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0.0014;
                                                                                            Length 1317;
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US-08-192-480A-2
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                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                  Sequence 52,
                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 42
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                  GENERAL
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                                                                             APPLICANT: Williams, Mark E.
APPLICANT: Stauderman, Kenneth A.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN CALCIUM
TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLATICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Richard J. Polley,
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatibl
OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CORRESPONDENCE ADDRESS:
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                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Andrew D. APPLICANT: Vandenbark
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ADDRESSEE:
ADDRESSEE:
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                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: Nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 121 S.W
CITY: Portland
ADDRESSEE: Heller Enrman warter Street: 4250 Executive Square, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Disk, 3-1/2 inch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                                                 INFORMATION:
                                                                                                                                                                                  2, Application US/08984709A 6320032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Richard J. Polley, Esq.
E: Klarquist Sparkman Campbell
E: Leigh & Whinston
121 S.W. Salmon Street, Suite 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       United States of America
                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
                             Heller Ehrman White & McAuliffe
                                                                                                                                                                                                                                                                                                                                                                   2.3%; Score 24;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polley, Esq.
ER: 28,107
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                                                                                                HUMAN CALCIUM CHANNEL COMPOSITIONS AND
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COUNTRY: US

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RESULT 11
US-08-984-709A-49/c
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; ORIGINAL SOURCE:
US-08-984-709A-52
                                                                                                                                                                                                                                                                                                                                                               Patent NO. USERVAL TORMATION:
GENERAL INFORMATION:
APPLICANT: Williams, Mark E.
APPLICANT: Stauderman, Kenneth A.
APPLICANT: Harpold, Michael M.
APPLICANT: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (619) 587-5360 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/984.
APPLICATION UNMER: US/08/984.
FILING DATE: 02-DEC-1997
CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: Seldman, Stephanie L.
REGISTRATION NUMBER: 33,779
REGISTRATION NUMBER: 33,779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                     SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,709A
FILING DATE: 02-DEC-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1313 CCTGGGCCTGGGCCTGGTG 1295
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 450-8400
                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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STRANDEDNESS: doub
TOPOLOGY: linear
                                                                                                                                                                     COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                 STATE:
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                           NAME: Seidman, Stephanie L. REGISTRATION NUMBER: 33,779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1413 base pairs
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: California
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             NUMBER:
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100.0%; Pred. No.
tive 0; Mismatc
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33,779
ER: 24735-9815 (formerly 6362-9815)
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13;
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US-09-114-146-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09114146 Patent No. 6083747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (619) 587-5360
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 460
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                       ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CI
HYPOTHETICAL: NO
ANTI-SENSE: NO
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: HAN, Xiaodong
TITLE OF INVENTION: GLYCOPROTEIN GP105 ON BLS HEMATOPOIETIC
TITLE OF INVENTION: STEM CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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nes 19; Conserv
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STRANDEDNESS: doub
                                                                         TELEFAX:
                                                                          TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
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 TYPE:
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             ENGTH:
nucleic acid
                                                          904136
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                                                                                                                                                                                                                                                                                                                                                                                                                                       3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHUNG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WONG, Peter M.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                 US/09/114,146
                                                                                                                                                                                                    08/471,188
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Best Local Similarity
Thes 18; Conserv
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                                                                                    US-08-934-386-1/c
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Best Local S
Matches 18
                                                       Sequence 1, Application US/08934386 Patent No. 6306636
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             GENERAL INFORMATION:
APPLICANT: Haselkorn, Robert
APPLICANT: Gornicki, Piotr
                                                                                                                                                                                                                                                                                                                                             TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 461
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                           685 tgctggggctgctggggcc 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247 TGCTGGGGCTGCTGGGCC 264
                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                     Local Similarity 100.0%; les 18; Conservative
                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20007-5109
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                                                                                                                                                                                                                                                                                                                                 410 base pairs
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(202)672-5399
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06-JUN-1995
                                                                                                                                                                                                                                                                                                      single
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Methods for Detecting Nucleic Acid
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Pred. No.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (512) 418-30 TELEFAX: (713) 789-2679 INFORMATION FOR SEQ ID NO:
                                                             OPERATING SYSTEM: DOS
SOFTWARE: FRASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/893,852A
FILING DATE: Filed Herewith
                                                                                                                                                                                                                                                                                               APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: NEW HUMAN GROWTH REGULATOR PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1645 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
                               PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: AF
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: SE NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESS:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   681 ctggtgctggggctgctg 698
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
ZIP: 77210-4433
                                                                                                                                                    COMPUTER:
                                                                                                                                                                                                       COUNTRY: U
ZIP: 94304
                                                                                                                                                                                                                                                     STREET: 3174 PO
CITY: Palo Alto
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TOPOLOGY: 11
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                                                                                                                                                                                                                                                                       ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                             , Application US/08893852A 6080558
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EDNESS: single
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P.O. Box 433
                                                                                                                                                                                                                       USA
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                                                                                                                                                E: Diskette
IBM Compatible
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19-SEP-1997
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Pred. No.
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REGISTRATION NUMBER:

36,749

Billings, Lucy J

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Query Match
Best Local Similarity
"-+ hes 18; Conserv
                                                                                     ; TOPOLOGY: 1
; MOLECULE TYPE:
US-08-279-270A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08279270A Patent No. 5691460 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                      TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDJUM TYPE: Floppy disk
COMPUTER: ITO COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
LIBRARY: TMLR3
CLONE: 508302
                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: WASYELD, Denise L.
REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: UTSH:173--1/MAY
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512,730-720
TELEPHONE: 512,7474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Duvic, Madeleine
APPLICANT: Schroeder, Wanda T.
TITLE OF INVENTION: Epidermal Surface Antigen and Uses
TITLE OF INVENTION: Thereof
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nes 18; Conservative (
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: Concur CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Houston
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                            1.7%; Score 18;
100.0%; Pred. No.
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                                          Length 2488;
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US-08-188-228-53
                                                                                                      RESULT 18
US-08-332-643-47/c
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                               Sequence 47, Application US/08332643
Patent No. 5639634
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 53, Application US/08188228 Patent No. 5597725
                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/872,64:
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2550 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Chicago
CITY: Chicago
TMATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION UNDER: US 08/049,460
PILLING DATE: 19 APR 1993
PRIOR APPLICATION UDDATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  990 GCCATCCTGGGCCTGGGC 973
                                                                                                                                                                                           663 gccatcctgggcctgggc 680
                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2550 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (312) 474-0448
TELEX: 25-3856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
                                                                                                                                                                                                                                               18;
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                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                 1.7%;
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                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                               Score 18;
; Pred. No.
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                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                 DB 1;
34;
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                                                                                                                                                                                                                                                                              Length 2550;
                                                                                                                                                                                                                                               Indels
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Gaps

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US-08-332-638-53/c
; Sequence 53, Applicat:
; Patent No. 5646250
; GENERAL INFORMATION:
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; MOLECULE TYPE:
US-08-332-643-47
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Best Local
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                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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NAME: NO. 56396348nd, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
                                                                                                                                                                                                                                               APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERI)
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/872,643
FILING DATE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           663 gccatcctgggcctgggc 680
                                                                                                                                                                                                                                                                                                                                                                                                                            990 GCCATCCTGGGCCTGGGC 973
APPLICATION NUMBER: US/0 FILING DATE: 01-NOV-1994
                                                                                                                                                                CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (312) 984-9740
TELEX: 25-3856
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                                                                                                                                                 COUNTRY:
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                                                                                                                                     60606
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                                                                                                                                                                                                                                                                                                                                             Application US/08332638
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6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                              Marshall, O'Toole, Gerstein, Murray &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Release #1.0, Version #1.25
                    US/08/332,638
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Pred. No.
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34;
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Best Local
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                                                                                                                            CLASSIFICATION: 435
ATTORIEY/AGENT INFORMATION:
ANAME: MUTHARD, DAVID A.
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 190.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                              TELEFAX: (908)594-4720 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 07065-9907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DESCRIPTION DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                              SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
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                             TYPE: nuclei
STRANDEDNESS:
                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: P.O. CITY: Rahway
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TOPOLOGY: 11n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (312) 474-0448
TELEX: 25-3856
              TOPOLOGY:
                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/872,643 FILING DATE: 17 APR 1992 APPLICATION NUMBER: US/08/049,460
                                                               LENGTH: 2647 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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18; Conserv
                                            nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                linear
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                               single
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FACTOR
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A NOVEL MAMMALIAN TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
34;
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Patent No
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/781,802
FILING DATE: 10-JAN-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/694,078
FILING DATE: 07-AUG-1996
CLASSIFICATION: 536
                                                                                                                                               TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3147 base pairs
TYPE: nucleic acid
STBANDEDURES: 5:5014
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APPLICATION NUMBER: US 60/001,995
FILING DATE: 01-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/009,704
FILING DATE: 11-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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APPLICATION NUMBER: US 60/019,580
FILING DATE: 12-JUN-1996
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                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis
                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                  NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                 LOCATION: 245..1231 OTHER INFORMATION:
                                                                                                                      STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 37,293
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   INFORMATION: INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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CASADABAN, Malcolm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FONSTEIN, Michael VONSTEIN, Veronika
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AIKENS,
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10-JAN-1997
                                                                                                                                  single
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100.0%; Pred. No.
tive 0; Mismatc
/note= "TspA E101 sequence longest
open reading frame; other possible start codons are TTG/leu9
TTG/leu13; TTG/leu15; GTG/val43"
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; NAME/KEY:
; LOCATION:
US-08-781-802-7
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US-08-694-078-7
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Best Local Similarity
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                                                                                                                                                                                         TELEFAX: 312-913-0002 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60,
FILING DATE: 12-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60,
FILING DATE: 10-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patenta...
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08
TING DATE: 07-AUG-1996
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                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 3147 base pairs
TYPE: nucleic acid
cTRANDEDNESCS: SIGNIA
                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: Chao, Mark
                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,995
FILING DATE: 07-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis
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                                                                              FEATURE:
                                                                                               MOLECULE TYPE:
NAME/KEY: CDS
LOCATION: 245..1231
OTHER INFORMATION: //
OTHER INFORMATION: O)
OTHER INFORMATION: T'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 300 S
CITY: Chicago
                                                                                                                                                                                                                                                                     NAME: Chao, Mark REGISTRATION NUMBER:
                                                                                                               TOPOLOGY:
                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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5218163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEMIRJIAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CASADABAN, Malcolm
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245..1231
                                                                                                              linear
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10-JAN-1996
                                                                                                                           single
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3, John
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100.0%;
/note= "TspA E101 sequence longest
open reading frame; other possible start codons are TTG/le
TTG/leu13; TTG/leu15; GTG/val43"
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                                                                                                                                                                                                                                                                      37,293
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Pred. No.
                                                                                                                                                                                                                                                        95,963-C
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US-09-058-260-7
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; LOCATION:
US-08-694-078-7
                                                                                      US-08-611-107-32/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: 60/001,995
EARLIER FILING DATE: 1996-08-07
EARLIER FILING DATE: 1996-01-11
EARLIER FILING DATE: 1996-01-11
EARLIER FILING DATE: 1996-01-12
EARLIER FILING DATE: 1996-06-12
EARLIER APPLICATION NUMBER: 08/694,078
EARLIER APPLICATION NUMBER: 08/781,802
EARLIER FILING DATE: 1996-08-08
EARLIER APPLICATION NUMBER: 08/781,802
EARLIER FILING DATE: 1997-01-10
EARLIER APPLICATION NUMBER: 08/827,810
EARLIER APPLICATION NUMBER: 08/827,810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-058-260-7; Sequence 7, Application US/09058260B; Patent No. 6218167
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APPLICANT: Alkens, John
APPLICANT: Fonstein, Wichael
APPLICANT: Vonstein, Veronika
APPLICANT: Demirjian, David
APPLICANT: Casadaban, Malcolm
                                Sequence 32, Applicat Patent No. 5801233 GENERAL INFORMATION:
                                                                                                                                                                                                                            Matches
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Best Local
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Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/058, 260B CURRENT FILING DATE: 1999-04-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis FILE REFERENCE: 95-963-H
                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence:cloned OTHER INFORMATION: gene from bacteria E101
                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: (24
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                           2214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ID NO 7
ENGTH: 3147
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                                                                 Application US/08611107
 Haselkorn, Robert
Gornicki, Piotr
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245..1231
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100.0%; Pr
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Pred. No.
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Pred. No.
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                                                                                                                                                                                                                                                            Sequence 2, Application US/08162146 Patent No. 5965788 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 18; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US SN 07/956,700
FILING DATE: 02-CCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/09340
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US SN 08/422,560
FILING DATE: 14-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
TERRATION NUMBER: 33,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (512) 474-7577 INFORMATION FOR SEQ ID NO:
                                                                                                                                             APPLICANT: HOUDEBINE, Louis-Marie
APPLICANT: DEVINOY, Eve
APPLICANT: THEPOT, Dominique
TITLE OF INVENTION: Production of a Protein of Interest in
TITLE OF INVENTION: the Milk of a Transgenic Mammalian
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                             2300 CTGGTGCTGGGGCTGCTG 2283
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
COMPUTER READABLE FORM
                                                                                                                            CORRESPONDENCE ADDRESS
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                   681 ctggtgctggggctgctg 698
                 COUNTRY: USA
ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                   CITY: Washington
                                                                                     ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Houston
STATE: Texas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 3243 base pairs
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E OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 18;
Pred. No.
                                                                                         Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
34;
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OPERATING SYSTEM:

3: Floppy disk IBM PC compatible SYSTEM: PC-DOS/MS-DOS

PatentIn Release #1.0, Version #1.30

MEDIUM TYPE:

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; LOCATION:
US-08-162-146-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09314127 Patent No. 6268545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 4157 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                           STREET: 5000
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                     APPLICANT: HOUDBBIRE, Louis-Marie
APPLICANT: DEVINOY, Eve
APPLICANT: THEPOT, Dominique
TITLE OF INVENTION: Production of a Protein of Interest in
TITLE OF INVENTION: the Milk of a Transgenic Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 25,258
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FR 91/07179 FILING DATE: 12-JUN-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/FR92/00533
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
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              PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 10-FEB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
                                CLASSIFICATION:
                                                 FILING DATE:
                                                                   APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                            20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WEGNER, Harold C.
                                                                                                                                                                                                                                                            E: Foley & Lardner
3000 K Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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..3429)
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08/162,146
                                                                 US/09/314,127
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                                                                                                                                                                                                                                                              Suite 500
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US-09-314-127-2
                                                                                        COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,107
FILING DATE: Concurrently Herewith
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US SN 07/956,700
FILING DATE: 02-OCT-1992
PRIOR APPLICATION NUMBER: US SN 07/956,700
FILING DATE: 02-OCT-1992
PRIOR APPLICATION NUMBER: US PCT/US93/09340
FILING DATE: 03-SEP-1993
PRIOR APPLICATION NUMBER: US PCT/US93/09340
FILING DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER: US N 08/422,560
FILING DATE: 11-TUTC/MTT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 30, Application US/08611107 Patent No. 5801233
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INFORMATION FOR SEQ ID NO:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
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ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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LENGTH: 4157 base pairs
                                  ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
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CORRESPONDENCE ADDRESS:
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APPLICANT: Gornicki, Piotr
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TELECOMMUNICATION INFORMATION:
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STRANDEDNESS: double
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                    REFERENCE/DOCKET NUMBER:
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18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Arnold, White & Durkee P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        United States of America
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100.0%; Pred. No.
/ative 0; Mismatc
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                    ARCD: 221
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US-08-905-223-270
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Best Local Similarity 100.0%;
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TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 30
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LENGTH: 316 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: DOUBLE
TOPOLOGY: LINEAR
                                                                                                                                                                                                                                                                                                            TELEFAX: (619) 235-0176 INFORMATION FOR SEQ ID NO: :
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MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WORD CURRENT APPLICATION DATA:
                                      NAME/KEY: other
LOCATION: 212..311
LOENTIFICATION WETHOD:
OTHER INFORMATION: iden
OTHER INFORMATION: reg-
OTHER INFORMATION: vrt
                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Edwards, Jean-Baptiste D.
APPLICANT: Duelert, Aymeric
APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
         NAME/KEY:
                                                                                                                                                                  ORGANISM: Homo Sapiens
TISSUE TYPE: Brain
                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Israelsen, Ned A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: California
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                                                      region 1..10
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                                                                                  identity 93
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Pred. No.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,818B
FILING DATE: 20-MAY-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03253
FILING DATE: 07-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 26, Applicat Patent No. 6261822 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                  APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: HYPERTHERMOSTABLE PROTEASE GENES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: FEATURE:
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IDENTIFICATION METHOD:
OTHER INFORMATION: 1den
OTHER INFORMATION: regi
OTHER INFORMATION: dd.
OTHER INFORMATION: est
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LOCATION: 179..250
IDENTIFICATION METHOD: Von Heijne matrix
OTHER INFORMATION: score 4.8
OTHER INFORMATION: seg ATMVSGSSGLAXA/RL
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OTHER INFORMATION:
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OTHER INFORMATION:
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IDENTIFICATION METHOD:
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5. 6261822
                                                                                                                                                                                                                                                                                                                                                                                           MITTA, Masanori
ASADA, Kiyozo
TSUNASAWA, Susumu
                                                                                                                                                                                                                                                                                                                                                                                                                                              MORISHITA, Mio
YAMAMOTO, Katsuhiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAKAKURA, Hikaru
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identity 100
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identity 91
region 5..63
id AA135265
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100.0%; Pred. No. 1.1e+02;
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id R58602
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APPLICATION NUMBER: JP 323285/1995 FILING DATE: 12-DEC-1995 ATTORNEY/AGENT INFORMATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER:

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NAME: Browdy, Roger L.

REGISTRATION NUMBER: 25,618
REGISTRATION NUMBER: TAKAKURA-1
REFERENCE/DOCKET NUMBER: TAKAKURA-1
TELECOMMUNICATION INFORMATION:
TELEPAX: (202) 628-5197
TELEPAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 507 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-894-818B-26
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; LOCATION: US-08-583-562B-5
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US-08-583-562B-5
                                                                                                       TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 545 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/08583562B Patent No. 5922570
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APPLICANT: Staunton, Donald
APPLICANT: Harris, Edith
TITLE OF INVENTION: Cytoplasmic Modulators of Integrin
TITLE OF INVENTION: Binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DC-DOS/MS-DOS
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                              CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DCKET NUMBER: 27866/33033
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,562B
FILING DATE:
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                                                                                    MOLECULE TYPE: CDNA
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STATE: Illinois
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Query Match 1.6%; Score 17; DB 2; L
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 0;
                                     Length 545;
    Indels
    0,
    Gaps
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밁 279 GGGCCTGGGGCTGAGCA 295

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71 gggcctggggctgagca 87

Search completed: June 19, 2002, 02:17:34 Job time: 3675 sec

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Title:
Perfect score:
Sequence:
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C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
C:Accession: 137552
R:Latza, U: Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fo
Eur. J. Immunol. 24, 677-683, 1994
A:Title: The human Ox40 homolog: cDNA structure, expression and chromosomal assignmen
A; Reference number: 137552; MUID:94170844
A; Accession: 137552
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-277 < CRES>
A; Cross-references: EMBL:X75962; NID:g472957; PIDN:CAA53576.1; PID:g472958
C; Superfamily: CD27 antigen; NGF receptor repeat homology
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\ensuremath{\mathsf{OX40}} antigen precursor - rat \ensuremath{\mathsf{N}}; \ensuremath{\mathsf{Alternate}} names: nerve growth factor receptor homolog
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## ALIGNMENTS

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Query Match 100.0%; Score 277; DB 2; I Best Local Similarity 100.0%; Pred. No. 2.5e-260; Matches 277; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                GPPARPITVQPTEAWPRTSQGPSTRPVEVPGGRAVAAILGLGLVLGLLGPLAILLALYLL
                                                                                                                                                                                                          NTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDSYK 120
                  RRDQRLPPDAHKPPGGGSFRTPIQEEQADAHSTLAKI 277
                                                                                                                                      PGVDCAPCPPGHFSPGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPATQPQETQ 180
                                                                     GPPARPITVQPTEAWPRTSQGPSTRPVEVPGGRAVAAILGLGLVLGLLGPLAILLALYLL
RRDQRLPPDAHKPPGGGSFRTPIQEEQADAHSTLAKI
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C;Accession: $12783; $508036
R;Mallett, S; Fossum, S; Barclay, A.N.
EMBO J: 9, 1063-1068, 1990
A;Title: Characterization of the MRC OX40 antigen of activated CD4 positive A;Reference number: $12783
A;Accession: $12783
A;Accession: $12783
A;Accession: $12783
A;Rolecule type: mRNA
A;Residues: 1-271 cMAL>
A;Cross-references: EMBL:X17037; NID:g57830; PIDN:CAA34897.1; PID:g57831
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: growth factor record repeat homology
C;Keywords: growth factor receptor; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <ATMM>
F;20-271/Product: OX40 antigen #status predicted <ATMM>
F;211-235/Domain: transmembrane #status predicted <ATMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL: 221674; NID:g312827; PIDN:CAA79772.1; PID:g312828
R;Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
Eur. J. Immunol. 25, 926-930, 1995
A;Title: Gene structure and chromosomal localization of the mouse homologue of rat OX40
A;Reference number: I48334; MUID:95255413
A;Accession: 148334
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: I-14, 'G', 16-272 < RE2>
A;Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819
C;Genetics:
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A;Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B (A;Reference number: 148700; MUID:94044750)
A;Accession: I48700
A;Accession: I48700
A;Status: translated from GB/EMBL/DDBJ
A;Residues: 1-272 <RES>
A;Residues: 1-272 <RES>
A;Cross-references: EMBL: Z21674; NID:q312827; PIDN:CAA79772.1; PID:g312828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene ox40 protein - mouse
N;Alternate names: OX40 antigen
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
C;Accession: I48700; I48334; S34377
C;Accession: I48700; I48334; S34377
hypothetical protein C2397 (photosynthetic gene cluster) - Rhodobacter capsulatus C;Species: Rhodobacter capsulatus C;Decies: Rhodobacter capsulatus C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Jun-1993 C!Accephiqn: F28771
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F28771
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C; Superfamily:
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D27 antigen; NGF receptor repeat
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                                                                                                                                                                                                                                                                                                         Score 12; DB; Pred. No. 0.0
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R;Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R. Nucleic Acids Res. 23, 2105-2119, 1995
A;Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region A;Reference number: S56314; MUID:95334362
A;Accession: S56343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
$56343
hypothetical protein f122 - Escherichia coli
n:Species: Escherichia coli
n:Species: One secouence_revision 03-No
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
C;Genetics:
A;Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Escherichia coli
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999
C;Accession: S56343
R;Burland, V:, Plunkett III, G:; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
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A;Title: Nucleotide and deduced polypeptide sequences A;Reference number: A90850; MUID:84259352
A;Accession: F28771
                                                                                         A; Experimental source: adult testis; clone DKFZp434N1535 C; Genetics: A; Note: DKFZp434N1535.1
                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-151 <AAA>
A; Cross-references: EMBL: AL133575
                                                                                                                                                                                             A; Reference number: Z;
A; Accession: T43478
A; Status: preliminary
                                                                                                                                                                                                                                                                                hypothetical protein DKFZp434N1535.1 - human (fragment) C;Species: Homo sapiens (man) C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #tex C;Accession: T43478
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""" B; Conserv
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A; Residues: 1-78 < YOU>
A; Cross-references: GB:K01183
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7, 1984
   Conservative
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LGLSTVTG 28

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MHC class II alpha chain - zebra fish C:Species: Brachydanio rerio (zebra fis C:Date: 13-Mar-1997 #sequence_revision C:Accession: I51740 R:Sultmann, H:; Mayer, W.E.; Figueroa, Immunogenetics 38, 408-420, 1993
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A; Authors: Smith, H.O.; Venter, J.C.
A; Title: Genomic sequence of a Lyme disease
A; Reference number: A70100; MUID:98065943
A; Accession: E70195
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son, D.; Peterson, J.
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A; Residues: 1-215 <WIL>
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A;Experimental source: strain B31
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                A; Title: Zebrafish
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, C.; Garland, S.;
, Ean-586, 1997
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MHC class II alpha chain-encoding: I51740; MUID:94011091
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                                             O'Huigin,
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                                                                                                                                                                                                                                                                 DB . 7
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                genes: polymorphism, expression,
                                              C.; Klein,
                                                                                                                                                                                                                                                  Indels
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                                                                             20-Sep-1999
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A; Accession: JH0749
A; Cross-references: GB:M95514; NID:g199312; PIDN:AAB46387.1; PID:g199313
A; Cross-references: GB:M95714; NID:g199312; PIDN:AAB46387.1
                                                                                                                                                                                                                                                                                                                                                                                                               R;Karlsson, L.; Peterson, P.A.
J. Exp. Med. 176, 477-483, 1992
A;Title: The alpha chain gene of
A;Reference number: JH0749; MUID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           class II histocompatibility antigen H-20 alpha chain precursor -
C;Species: Mus musculus (house mouse)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change :
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A; Residues: 1-236 <SUL>
A; Cross-references: GB:L19446; NID:g311194;
A; Accession: 151745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: JH0749
R; Karlsson, L.; Pete
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A; Residues: 1-236 <SU2>
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A; Accession: I51741
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A;Title: Zebrafish MHC class II alpha chain-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            c:Date: 13-Mar-1997 #sequence_revision
C:Accession: I51741; I51745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Brachydanio rerio (zebra
C;Date: 13-Mar-1997 #sequence_revis:
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A; Residues: 1-236 <SUL>
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A;Accessium: November 1975
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-315 <KUR>
A;Cross-references: GB:BA000018; PID:g13700972; PIDN:BAB42268.1; GSPDB:GN00149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conserved hypothetical protein SA1016 [imported] - Staphylococcus aureus (strain N3: C;Species: Staphylococcus aureus C;Species: Staphylococcus aureus C;Date: 10-May-2001 **sequence_revision 10-May-2001 **text_change 22-Oct-2001 C;Accession: H89888 R;Kuroda, M; Ohta, T.; Uchyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; R; Kuroda, M; Ohta, T.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 125-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A; Reference number: A89758; MUID:21311952; PMID:11418146
                               RESULT
S17765
                                                                                                                                                                                                                                                                                                      R:Coleman, G.D.; Chen, T.H.H.
submitted to the EMBL Data Library,
A:Reference number: S31580
A:Accession: S31580
A:Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                    storage protein, bark - cottonwood
c;Speckes: Populus deltoides (cottonwood)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
C;Accession: S31580
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S31580
 c; Species
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A;Residues: 1-329 <COL>
A;Cross-references: EMBL:X70064; NID:g20464; PID:g20465
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(Carolina poplar)
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AALLLLGL 287

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RESULT
C36942
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1
C;Accession: S17765; S25320
R;Clausen, S; Apel, K.
Plant Mol. Biol. 17, 669-678, 1991
A;Title: Seasonal changes in the concentration
A;Reference number: S17765; MUID:92003681
A;Accession: S17765
A;Status: preliminary
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                                                                                                                                     A; Gene: PA4219
C; Superfamily:
                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-394 <STO>
A;Cross-references: GB:AE004838; GB:AE004091; NID:g9950422; PIDN:AAG07607.1; GSPDB:GN
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:U03161; NID:g454352; PIDN:AAC43215.1; PID:g454355 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Fadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Ankenbauer, R.G.; Quan, H.N.
J. Bacteriol. 176, 307-319, 1994
A;Title: FptA, the Fe(III)-pyochelin receptor of Pseudomonas aeruginosa: a phenolate A;Reference number: A36942; MUID:94117363
A;Accession: C36942
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A;Molecule type: mRNA
A;Residues: 15-19 <CL;
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A;Note: the authors translated the codon GTG for residue
A;Note: the nucleotide sequence has been revised in refe
R;Clausen, S.; Apel, K.
Plant Mol. Biol. 20, 365, 1992
A;Tille: Seasonal changes in the concentration of the mata, Reference number: S25320; MUID:93004495
                                                                                                                                                                                                                                                                                               A; Title: Complete genome sea
A; Reference number: A82950;
A; Accession: G83119
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A; Residues: 1-394 < ANK>
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A; Residues: 1-329 < CLA>
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A.; Larbig, K.; L
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C; Accession: D83106
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguch, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; I F. Lory, S.; Olson, M.V.; Nature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas A; Reference number: A82950; MUID: 20437337
A; Accession: D83106
                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE000484; GB:U00096; NID:g2367352; PIDN:AAC77076.1; PID:g2367353; A;Experimental source: strain K-12, substrain MG1655
R;Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 23, 2105-2119, 1995
A;Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.
A;Reference number: S56314; MUID:95334362
A;Accession: S56314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable amino acid/amine transport protein [similarity] - Escherichia coli (strain K-12 N;Alternate names: hypothetical protein f326a C;Species: Escherichia coli (strain K-12 C;Species: Escherichia coli (strain K-12 C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 02-Nov-2001 C;Accession: B65221; S56344
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CC.A.; Rose, D.J.; Mau, B.; Shao, Y.
RESULT
A91266
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A; Residues: 1-321, 'SQWR', 326 <BUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia A;Reference number: A64720; MUID:97426617
A;Accession: B65221
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A; Residues: 1-445 <BLAT>
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A; Residues: 1-443 <STO>
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L.L.; Coulter, S.N.; Folger,
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, K.R.; Kas,
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gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Accession: A91266
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R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
                                                                                                                                                                                   A; Gene: yjdE
C; Superfamily: L-lysine transport protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable amino acid/amine transport protein [similarity] -
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_ch
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A; Residues: 1-445 <HAY>
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A; Residues: 1-445 <STO>
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Matches 8; Conser
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                                       13 CAALLLLG
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CAALLLLG
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Conservative (
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ilarity 100.0%;
Conservative
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376
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                                                                             %; Score 8; DB 2
%; Pred. No. 14;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 8;
Pred. No.
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                                                                                                                       2;
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RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                           B.; Glasner,
imalanta, E.;
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                                                                               0,
                                                                                                                       Length 445;
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Potamousis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-Nov-2001
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probable amino acid permease STY4493 [imported] - Salmonella enterica subsp. C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 27-Nov-2001

enterica

AF1022

RESULT

20

Nature 413, 848-852, 2001 A;Authors: Parry, C.; Quail, M.; F A;Title: Complete genome sequence

Quail, M.; Rutherford, K.; Simn ome sequence of a multiple drug

Simmonds, M.; drug resistant

Skelton, J.; Salmonella e

enterica

se

S.; Moule, S.; O'Ga ature 413, 848-852,

O'Gaora, P. 852, 2001

T.; Connerton,

P.; Cronin,

; James, nin, A.;

K.D.;

Thomson, N.R., P.; Davies,

N.R.; Pickard, D.; Wain, J.; Church ies, R.M.; Dowd, L.; White, N.; Farr

C;Accession: AF1022 R;Parkhill, J.; Dougan, G.;

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A;Reference number: AB05
A;Accession: AF1022
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-445 <PAR>
                                                                                                                                                                                        acyl-CoA synthase [imported] - Mycobacterium leprae C:Species: Mycobacterium leprae C:Species: Mycobacterium leprae C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 15-Jun-2001 C:Accession: B87040 R:Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Whee: R: Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, eam, M.A.; Rutherford, K.M. Nature 409, 1007-1011, 2001
A.Authors: Rutter, S.; Seger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squareries.
                                                   A; Status: preliminary A; Molecule type: DNA A; Residues: 1-476 <STO
                                                                                                                                               A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; A;Title: Massive gene decay in the leprosy bacillus. A;Reference number: A86909; MUID:21128732; PMID:11234002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable fadD36 protein - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

C;Accession: G70607

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.;

Connor, R.; Davies, R.; Deviln, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complet

A;Reference number: A70500; MUID:98295987
                                                                                                                        A; Reference number: A86909; A; Accession: E87040
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C;Superfamily: 4-coumarate--CoA ligase; acetate--CoA
F;42-469/Domain: acetate--CoA ligase homology <ACL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-473 <COL>
A;Cross-references: GB:Z93777; GB:AL123456; NID:g3261726; PIDN:CAB07836.1; PIDA:Experimental source: strain H37RV C;Genetics:
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C;Superfamily: L-lysine transport protein
                         A;Cross-references: GB:AL450380; NID:g13093059; PIDN:CAC31432.1; GSPDB:GN00147
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; GB:AL123456; NID:g3261726; PIDN:CAB07836.1; PID:g1929067
H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 8; DB 2; Pred. No. 15; 0; Mismatches
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Pred. No.
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14;
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Holroyd,
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                                                                                                                                                                                                   R.,
A;Cross-references: GB:Z99123; GB:AL009126; NID:g2636240; PIDN:CAB15899.1; PID:e11863
A;Experimental source: strain 168
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A; Experimental:
C; Genetics:
A; Gene: SP1328
                                                                                                                                                                                                                                                                                                                                                                                                                                      on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, I nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001

Righthors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus A;Reference number: A95000; MUID:21357209; PMID:11463916

Righthory Complete Genome Sequence of PMID:11463916
                 C; Species: Bacillus subtilis
C; Date: 05-Dec-1997 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sodium/solute symporter family protein [imported] - Streptococcus pneumoniae C;Species: Streptococcus pneumoniae C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
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C;Superfamily: 4-coumarate--CoA ligase; acetate--CoA ligase homology
C; Accession: D69611
                                                     ABC transporter
                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-513 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Tettelin, H.; Nelson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession:
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Best Local
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Best Local !
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8; Conserv
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                 nces: GB:AE005672; PIDN:AAK75426.1;
source: strain TIGR4
                                                    required for expression of cytochrome bd (ATP-)
                                                                                                                                                                                                                     Conservative
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White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzappl
Holt, I.E.
                                                                                                                                                                                                                                       2.9%;
100.0%;
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Pred. No.
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Pred. No.
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                 05-Dec-1997 #text_change
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. 15;
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15;
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                   02-Feb-2001
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R;Knst, F; Ogasawara, N; Moszer, I; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galiech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Se Reche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Se akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A.; Althors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A.; Reference number: A69580; MUID:98044033 A; Molecule type: DNA A; Residues: 1-575 < KUN> A;Status: preliminary; nucleic acid sequence not shown; A; Reference number: A; Accession: D69611 translation not

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alpha,alpha-trehalase (EC 3.2.1.28) - human
C;Species: Homo sapiens (man)
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 20-Jun-2000
C;Accession: JC6504
R;Ishihara, R; Taketani, S; Sasai-Takedatsu, M; Kino, M; Tokunaga, R; Kobayashi, Y, Gene 202, 69-74, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNĀ
A; Residues: 1-578 < TUPS
A; Cross-references: GB: M55299; NID: g164736;
C; Superfamily: human alpha, alpha-trehalase
C; Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: cydD (;Superfamily: unassigned ATP-binding cassette proteins; C;Keywords: ATP; nucleotide binding; P-loop F;353-946/Domain: ATP-binding cassette homology <ABC>F;370-377/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-583 <ISH>
A; Cross-references: DBJ:AB000824; NID:g2789460;
C; Superfamily: human alpha, alpha-trehalase
C; Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                              Gene 202, 69-74, 1997
A;Title: Molecular cloning, sequencing and
A;Reference number: JC6504; MUID:98087419
A;Accession: JC6504
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JC6504
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A;Title: Rabbit small intestinal trehalase. Purification, A;Reference number: A35810; MUID:90368681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alpha,alpha-trehalase (EC 3 2.1.28) precursor - rabbit C; Species: oryctolagus cuniculus (domestic rabbit) C; Date: 23-oct-1990 #sequence_revision 23-oct-1990 #text_change 02-Jun-2000 C; Accession: A35810
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LLLIGLGL 18
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hypothetical protein KIAA0527 - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000
C;Accession: T00073
R.Nagase, T; Ishikawa, K; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, DNA Res. 5, 31-39, 1998
A;Title: Prediction of the coding sequences of unidentified human genes. IX. The comp A;Reference number: Z14086; MUID:98290545
A;Accession: T00073
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
A;Gene: ATSP:F23E12.170
A;Map position: 4
A;Introns: 307/3; 359/2; 682/1; 898/3; 962/1
C;Superfamily: Arabidopsis thaliana hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: T06130
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, submitted to the Protein Sequence Database, April 1999
A;Reference number: Z15485
A;Accession: T06130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F23E12.170 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 15-Sep-2000
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A; Residues: 1-768 < NAGE
A; Cross-references: EMBL: AB011099; NID:g3043577;
A; Experimental source: brain; clone HG2246
C; Genetics:
A; Accession: T01742
A; Status: preliminary;
A; Molecule type: DNA
A; Residues: 1-52 <SMI>
                                                                             R;Smith, A.G.; Pring, D.R.
Curr. Genet. 12, 617-623, 1987
Curr. Wolleotide sequence and molecular
A;Reference number: Z14414; MUID:89003167
                                                                                                                                                          C:Species: mitochondrion Zea mays (maize)
C:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999
C:Accession: T01742
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A;Residues: 1-1031 <BEV>
A;Cross-references: EMBL:AL022604; GSPDB:GN00062; ATSP:F23E12.
A;Experimental source: cultivar Columbia; BAC clone F23E12
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21;
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C:Species: Enterobacter aerogenes plasmid R751
C:Species: Enterobacter aerogenes
C:Species: Enterobacter aerogenes
C:Species: Enterobacter aerogenes
C:Date: 11.Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Ju1-2000
C:Accession: T08512
R:Thorsted, P.B.; Shah, D.S.; Macartney, D.; Kostelidou, K.; Thomas, C.M.
Plasmid 36, 95-111, 1996
A:Title: Conservation of the genetic switch between replication and transfer genes of In A; Reference number: Z16434; MUID:97118926
A; Reference number: T08512
A; Scatus: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-88 <THO>
A; Conservation of the genetics: EMBL:U67194; NID:g1572520; PIDN:AAC64456.1; PID:g1572561
C:Genetics: TDO
A; Conservation of the genetics: EMBL:U67194; NID:g1572520; PIDN:AAC64456.1; PID:g1572561
C:Genetics: TDO
Search completed: June 18, 2002, 14:29:51 Job time: 209 sec
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                                                                                                                                                                                                                                                                                                                                                                                       A; Genome: plasmid R751
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7 2.5 373 1 YLUZ_PICAN 7 2.5 389 1 YSG_MYCTU 7 2.5 389 1 YSG_MYCTU 7 2.5 415 1 CRF1_MOUSE 7 2.5 415 1 CRF1_MOUSE 7 2.5 415 1 CRF1_RAT 7 2.5 415 1 CRF1_RAT 7 2.5 428 1 NSD1_PSEAE 7 2.5 441 1 ODBA_MOUSE 7 2.5 441 1 ODBA_MOUSE 7 2.5 444 1 ODBA_MOUSE 7 2.5 444 1 CRF1_HUMAN 7 2.5 446 1 YBO_THETH 7 2.5 469 1 NQOD_THETH 7 2.5 498 1 YBO_THETH 7 2.5 548 1 ERF_MOUSE 7 2.5 548 1 ERF_MOUSE 7 2.5 548 1 ERF_MOUSE 7 2.5 548 1 ALIGNMENTS	2	
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1 YLUZ_PICAN 1 Y4MD_RHISN 1 Y49MD_RHISN 1 Y596_MYCTU 1 CRF1_MOUSE 1 CRF1_MOUSE 1 CRF1_RAT 1 CRF1_PSEAE 1 MNT2_PSEAE 1 ODBA_MOUSE 1 ODBA_MOUSE 1 ODBA_MOUSE 1 CRF1_HUMAN 1 YBO7_HAEIN 1 WODD_THETH 1 NFS1_SCHPO 1 ERF_HUMAN 1 ERF_MOUSE 1 ERF_MOUSE 1 ERF_MOUSE ALIGNMENTS	371	
YLUZ_PICAN YAWD_RHISN YAWD_RHISN YS96_MYCTU YS96_MYCTU CRF1_MOUSE CRF1_SHEEP NSD1_PSEAE MNT2_PSEAE MNT2_PSEAE ODBA_RAT ODBA_RAN CRF1_HUMAN YB07_HAEIN NQOD_THETH NQOD_THETH NQODAN MFS1_SCHPO ERF_HUMAN ERF_MOUSE ALIGNMENTS	_	
	Y4OS RHISN	
P34735 P556837 Q10817 Q10817 P35347 P353753 O627753 O9hyl1 Q9hyl1 Q9hyl1 P50136 P50136 P50136 P50136 P50136 P50148 P704351	P55604	
	rhizobium	

## TNR4\_HUMAN STANDARD; PRT; 277 AA. P43489; Q13663; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Tumor necrosis factor receptor superfamily member 4 precursor (OX40L receptor) (ACT35 antigen) (TAX-transcriptionally activated glycoprotein 1 receptor) (CD134 antigen). EMBL; X75962; EMBL; S76792; HSSP; P25942; SEQUENCE FROM N.A. MEDLINE=94170844; PubMed=7510240; Latza U., Duerkop H., Schnittger S., Ringeling J., Eitelbach F., Hummel M., Fonatsch C., Stein H.; "The human 0x40 homolog: cDNA structure, expression and chromosomal assignment of the ACT35 antigen."; Eur. J. Immunol. 24:677-683(1994). use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstati the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NCBI\_TaxID=9606; SEQUENCE FROM N.A. DATABASE: NAME-PROW; NOTE-CD guide CD134 entry; WWW-"http://www.ncb1.nlm.nih.gov/prow/cd/cd134.htm". 600315 1CDF. AAB33944.1; CAA53576.1; ALT\_INIT Euteleostomi; a collaboration R.A., M.R.; of

Pro; IPR001368; TNFR\_c6. PF00020; TNFR\_c6; 3.

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RESULT
TNR4_RAT
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Best Local Similarity
Matches 277; Conser
            TISSUE-T-cell;

MEDLINE-90214614; PubMed=2157591;

Mallett S., Fossum S., Barclay A.N.;

"Characterization of the MRC OX40 antigen of actival Characterization of the MRC OX40 antigen of actival Lymphocytes -- a molecule related to nerve growth filemed J. 9:1063-1068(1990).

EMBO J. 9:1063-1068(1990).

-I- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.

-I- SUBCELLULAR LOCATION: Type I membrane protein.

-I SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
CARBOHYD
CARBOHYD
SEQUENCE
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REPEAT
REPEAT
REPEAT
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TRANSMEM
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PROSITE;
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                                                                                                                                                                                                                                     TNR4_RAT P15725;
                                                                                                                                                             01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor superfamily member receptor) (OX40 antigen) (MRC OX40).
TNFRSF4 OR TXGPIL OR OX40.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                NCBI_TaxID-10116;
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         SIMILARITY: CONTAINS 4 THER-CYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                    NTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDSYK
                                                                                                                                                                                                                                                                                                                                                                                                                         NTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDSYK
                                                                                                                                                                                                                                                                                                                                                                                  PGVDCAPCPPGHFSPGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPATQPQETQ
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re; PS50050;
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236
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66
108
127
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TNFR_NGFR_2; 2.
Antigen; Glycoprotein;
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235
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TUMOR NECROSIS FACTOR REC
SUPERFAMILY MEMBER 4.
EXTRACELLULAR (POTENTIAL)
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3 (INCOMPLETE).
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N-LINKED (GLCNAC. . .) (POTENTIAL)

N-LINKED (GLCNAC. . .) (POTENTIAL)

LINKED (GLCNAC. . .) (POTENTIAL)

49F15525941550BF CRC64;
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Pred. No. 2.6
); Mismatches
                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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         REPEATS.
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2.6e-263;
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TNR4_MOUSE
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Best Local S
Matches 12
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P47741;

01-FEB-1996 (Rel. 33, Created)

10-FEB-1996 (Rel. 33, Last sequence upda

11-CCT-2001 (Rel. 40, Last annotation up

""""" necrosis factor receptor superfam!
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TRANSMEM
DOMAIN
REPEAT
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REPEAT
CARBOHYD
SEQUENCE
                        MEDLINE-95255413; PubMed-7737295; MEDLINE-95255413; PubMed-7737295; Gilbert
                  Birkeland M.L.,
Barclay A.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SMUUJUU; III..., PROSITE; PS00652; TNFR_NGFR_1; 3.
PROSITE; PS50050; TNFR_NGFR_2; 2.
PROSITE; PS50050; Antigen; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00020; TNFR_C6; 3.
ProDom; PD000771; TNFR_C6; 1.
SMART; SM00208; TNFR, 36;
PROSITE; PS00652; TNFR_NGFR_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; x17037; CAA34897.1; -. PIR; S08036; S08036. PIR; S12783; S12783. HSSP; P19438; 1EXT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                      Calderhead D.M., Buhlmann J.E., va
Claassen E., Noelle R.J., Fell H.;
"Cloning of mouse Ox40: a T cell a
T-B cell interactions.";
                                                                                                                                                                                                             receptor) (OX40 antigen).
TNFRSF4 OR TXGP1 OR OX40.
Mus musculus (Mouse).
                                                                                                                                              SEQUENCE FROM N.A. STRAIN=BALB/C;
                                                                                                                                                                            Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
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           "Gene
                                                                             J. Immunol.
                                                                                                                                 MEDLINE=94044750; PubMed=8228223;
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 rat
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 structure
COX40 prot
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12; Conser
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236
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103
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271,
ture and protein.
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ilarity 100.0%;
Conservative
                                                                             151:5261-5271(1993).
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271
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Rodentia;
  chromosomal
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EXTRACELLULAR (POTEN
POTENTIAL.
CYTOPLASMIC (POTENT
TNER-CYS 1.
TNER-CYS 2.
                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 12;
Pred. No.
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N-LINKED (GLCNAC...) (P
C06465136B16EB21 CRC64;
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otation update)
superfamily member 4 precursor (0x40L)
            localization
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                                D.J.,
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            of the
                                 Jenkins
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                                                                                                                        А.J.,
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            mouse homologue
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Best Local
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TR11_MOUSE STANDARD; PR

C03505;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last seque

01-MAR-2002 (Rel. 41, Last annot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X85214; CAA59476.1; -.
HSSP; P19438; LEXT.
MGD; MGI:104512; Tnfrsf4.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 3.
ProDom; PD000771; TNFR_c6; 1.
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CONFLICT
SEQUENCE
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SIGNAL
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                                 TISSUE=Fetal liver;
MEDLINE=98032977; PubMed=9367155;
Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.
Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D
Galibert L.;
                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                          Tumor necrosis factor receptor superfamily member 11A precursor Receptor activator of NF-KB) (Osteoclast differentiation factor receptor) (ODFR).

TNFRSF11A OR RANK.
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REPEAT
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REPEAT
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SMART; SM00208; TNFR; 3.
PROSITE; PS000652; TNFR_NGFR_1
PROSITE; PS50050; TNFR_NGFR_2
                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                             Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 NQACKPWTNCTL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                               136
                homologue of the TNF receptor and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . J. Immunol. 25:926-930(1995).
FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: CONTAINS 4 THER-CYS REPEATS.
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TNFR_NGFR_2; 2.
Antigen; Glycoprotein; Transmembrane; Repeat;
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Rodentia;
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Last annotation update)
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TNFR-CYS
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06E7BB4156F0D08E
                its ligand enhance T-cell growth
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RESULT 5
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DOMAIN
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- PROCTION: RECEPTOR FOR RANK LIGAND (RANKL; ALSO KNOWN AS OSTEOCLAST DIFFERENTIATION FACTOR OR ODF), ESSENTIAL FOR RANKL-MEDIATED OSTEOCLASTOGENESIS. INVOLVED IN THE REGULATION OF INTERACTIONS BETWEEN T-CELLS AND DENDRITIC CELLS.

- SUBCELLULAR LOCATION: Type I membrane protein (Potential).

- TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEVELS IN TRABECULAR BONE, THYMUS, SMALL INTESTINE, LUNG, BRAIN AND KIDNEY.

WEAKLY EXPRESSED IN SPLEEN AND BONE MARROW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:1314891; Tnfrsfila.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 3.
ProDom; PD000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Morinaga T., Higashio K.;
"RANK is the essential signaling receptor for osteoclast differentiation factor in osteoclastogenesis.";
PUFX_RHOCA STANDARD:
P26240;
01-MAY-1992 (Rel. 22, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF019046; AAB86810.1; HSSP; P25942; 1CDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00652; TNFR_NGFR_1: 1.
PROSITE; PS50050; TNFR_NGFR_2; 1.
Receptor; Glycoprotein; Transmemb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakagawa
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                                                                                                           CKPWTNCTL 178
                                                                                                                                                                    Similarity
9; Conserv
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CYTOPLASMIC (POTENTIAL).
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P42514;
O1-NOV-1995
O1-NOV-1995
16-OCT-2001
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SEQUENCE FROM N.A. STRAIN-ATCC 15692 MEDLINE-20437337;
                                                                 phenolate siderophore receptors.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Photosynthesis;
SEQUENCE 78 AJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Youvan D.C., Bylina E.J., Alberti M., Begusch "Nucleotide and deduced polypeptide sequences reaction-center, B870 antenna, and flanking pocapsulata.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-84259352; PubMed-6744416;
RVIINA E.J., Alberti,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhodobacter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhodobacter capsulatus
                                                                                    Ankenbauer R.G., Quan H.N.; "ptA, the Fe(III)-pyochelin receptor of Pseudomonas aeruginosa:
                                                                                                            MEDLINE-94117363; PubMed-8288523;
                                                                                                                          STRAIN-PAO;
                                                                                                                                                                                    Bacteria; Proteobacteria;
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15-JUL-1998 (Rel.
                                                               receptors
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                                                                                                                                                                          Pseudomonas
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                                                  Bacteriol.
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SUBCELLULAR LOCATION: INTRACYTOPLASMIC MEMBRANE.
SIMILARITY: TO PUFY FROM R.SPHAEROIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 37:949-957(1984).

FUNCTION: ASSOCIATED WITH THE REACTION CENTER - LIGHT-HARVESTING COMPLEX I. MAY PLAY A CRITICAL ROLE IN FACILITATING THE
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F28771; F28771.
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  PubMed=10984043;
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               PAO1;
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                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Created)
15-JUL-1998 (Rel. 36, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Hypothetical transport protein yjdE.
YJDE OR B4115 OR 25717 OR ECS5097.
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       Gregor J.,
                                                                                                                            SEQUENCE FROM N.A.
STRAINER12 / MG1655;
MEDLINE-95334362; PubMed-7610040;
Burland V.D., Plunkett G. III, Sofia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U03161; AAC43215.1; -
EMBL; AE004838; AAG07607.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an
                                                                                                                                                                                                               Escherichia coli, and Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities
                                                                                   "Analysis of the Escherichia coli genome region from 92.8 through 100 minutes."; Nucleic Acids Res. 23:2105-2119(1995).
                                                                                    Nucleic
                                                                                             region
                                                                                                                    Blattner F.
                                                                                                                                                                                 NCBI_TaxID=562, 83334;
                                                                                                                                                                                             Escherichia
                                                                                                                                                                                                      Bacteria;
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European Bioinformatics Institute.
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Davis
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         Kirkpatrick
                 G. III, Bloch C.A., Perna N.T., Burl
J., Glasner J.D., Rode C.K., Mayhew
                                                                                                                                                                                                                                                                                                                                                                                                          .08;
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EMBL; U14003; AAA97014.1; ALT_FRAME.
EMBL; AE000484; AAC77076.1; --
EMBL; AE005644; AAG59314.1; --
EMBL; AP002568; BAB38520.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                             SEQUENCE
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InterPro; IPR002027; Amino_acid_permeas
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0157:H7 and genomic comparison with a laboratory strain K-12.";
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Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-0157:H7 / EDL933 / ATCC 700927; MEDLINE-21074935; PubMed-11206551;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Integral membrane protein.
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            CAALLLLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complete genome sequence of Escherichia coli K-12.";
see 277:1453-1474(1997).
CAALLLLG
                                              n 2.9%;
Similarity 100.0%;
8; Conservative
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TREA_RABIT P19813;
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TRANSMEM
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ATP-binding;
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequencing of a 65 kb region of the Bacillus subtilis ger containing the lic and cel loci, and creation of a 177 kb covering the gnt-sacXY region."; microbiology 142:3113-3123(1996).

-i-FUNCTION: SOMEHOW INVOLVED IN THE CYTOCHROME D BRANCH RESPIRATION. SEEMS TO BE A COMPONENT OF A TRANSPORT SY SIMILARITY).
                                                                                                                                                                 TRANSMEM
NP_BIND
SEQUENCE
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                                                                                                                                                                                                                                                                                                            InterPro;
InterPro;
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P94367;
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MEDLINE=97124196;
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Bacteria; Firmicut
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                                                                                                                                                                                                                                                                             SMART; SM00382;
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NCBI_TaxID=1423;
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                                                                  160
                                                                                      232 AILLALYL 239
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                                                                 AILLALYL
                                                                                                                                                                                                                                                                                     PF00664; ABC_membrane; PF00005; ABC_tran; 1.
                                                                                                           8;
                                                                                                                    Similarity
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IPRO01140; ABC_transporter_tmem.
IPRO03439; ABC_transportr.
IPRO01687; ATP_GTP_A.
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17 37
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135 155
161 181
246 266
275 295
370 377
                                                                                                           Conservative
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            STANDARD;
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41,
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indo K., Sano H.,
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O43280;
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01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Trehalase precursor (EC 3.2.1.28) (Alpha,alpha-trehalase)
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Trehalase precursor (EC 3.2.1.28) (Alpha, alpha-trehalase)
(Alpha,alpha-trehalose glucohydrolase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -I- FUNCTION: INTESTINAL TREHALASE IS PROBABLY INVOLVED IN THYDROLYSIS OF INGESTED TREHALOSE.
-I- CATALYTIC ACTIVITY: Alpha, alpha-trehalose + H(2)O = 2 D-
-I- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
-I- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-
-I- TISSUE SPECIFICITY: SMALL INTESTINE, KIDNEY, AND LESSER
-I- SIMILARITY: BELONGS TO FAMILY 37 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Ve; Mammalia; Eutheria; Lagomorpha; Leporidae; NCBI_TaxID=9986;
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von Kieckebusch A., Semenza G., Mantei N.;
"Rabbit small intestinal trehalase. Purifi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND F
STRAIN-NEW ZEALAND WHITE;
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cuniculus (Rabbit).
matazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
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Homo sapiens (Human).
Tharvota; Metazoa; Chordata; Cr
                   NULM_BRALA STANDARD; PRT; 91 AA 079420; 047424; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) 15-DEC-1998 (Rel. 37, Last annotation
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Pfam; PF01204; Trehalase; 1.
PRINTS; PR00744; GLHYDRLASE37.
PROSITE; PS00927; TREHALASE_1;
PROSITE; PS00928; TREHALASE_2;
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MEDLINE-9636935; Pubmed-8773341;
MEDLINE-9636935; Pubmed-8773341;
Medani S., Nagata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        trehalase."
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583 AA; 665961
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GPI-ANCHOR (BY SIMILARITY).

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         1.6.5.3)
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MEDLINE-89139485; PubMed=2917992;
MEDLINE-89139485; PubMed=2917992;
Oquendo P., Alberta J., Wen D., Graycar J.L., Derynck R., Stil
Oquendo P., Alberta J., Wen D., Graycar J.L., Derynck R., Stil
"The platelet-derived growth factor-inducible KC gene encodes
"The platelet-derived growth factor-inducible KC gene encodes
"The platelet alpha-granule proteins."
                                                                                                                                                                                      GRO_MOUSE STANDARD; PRT; 96 AA. p12850; 01-OCT-1989 (Rel. 12, Created) 01-OCT-1989 (Rel. 12, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Growth regulated protein precursor (Platelet-derived inducible protein KC) (Secretory protein NS1). SCYB1 OR GRO1 OR GRO OR MGSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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the Euro
                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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InterPro; IPR003214; Mit_NADHub_oxidredctse_4L.
InterPro; IPR001133; Oxidored_q2.
Pfam; PF00420; oxidored_q2; 1.
ProDom; PD000359; Mit_NADHub_oxidredctse_4L; 1.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 91 AA; 9751 MW; 7E7D093F02468BD3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spruyt N., Delarbre C., Gachelin G., Laudet V.; "Complete sequence of the amphioxus (Branchiostoma lanceolatum) mitochondrial genome: relations to vertebrates."; Nucleic Acids Res. 26:3279-3285(1998).
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MEDLINE-99261652; P
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Mol. Biol. E
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MEDLINE=98292550; PubMed=9628930;
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Sciurognathi; Muridae;
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EMBL; U20634; AAB03376.1; -.
EMBL; U20527; AAB03376.1; JOI
EMBL; S79767; -; NOT_ANNOTATE
PIR; A32954, 32954.
PIR; JH0081; JH0081.
HSSP; P19875; 1QNK.
ELAB_ECOLI ST/
P52084; Q47010;
01-OCT-1996 (Rel.
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Conklyn M.J., Breslow R., Showell
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Ryseck R.P., Macdonald-Bravo
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InterPro; IPR001089; Small_cytokine_CXC
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onald-Bravo H.,
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Pred. No.
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l H.J., Gerard N.P., Gerard C.;
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01-NOV-1997 (Rel. 16-OCT-2001 (Rel.

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STRAIN-0157:H7 / RIMD 0509952;

MEDLING-21156231; PubMed-11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya
Hayashi T., Makino E., Nakayama K., Murata T., Tanaka M., Tobe T
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunac
Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                  STRAIN-0157:H7 / EDL933 / ATCC 700927;

MEDLINE-21074935; PubMed-11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;
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Escherichia coli 0157:H7.
Bacteria; Proteobacteria;
Rudd K.E.;
Unpublished observations
-|- SIMILARITY: STRONG, T
                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=K12 / MC4100;

MEDLINE=96140724; PubMed=8549818;

Mueller R., Dahm C., Schulte G., Leistner E.;

"An isochorismate hydroxymutase isogene in Es:

"EBS Lett. 378:131-134(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - K12 genome corresponding to 50.0-6 analysis of its sequence features."; DNA Res. 4:91-113(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamaamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K., Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N., Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H., Oshina T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S., Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C., Yamagata S., Horiuchi T.;
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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ELAB OR B2266 OR Z3526
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                                                                                                                                                                                                                                                                                                 NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
PIR; B24560; HSDU1B.
HSSP; P02259; 1HST.
                                                                                                                                                                                                                                                                                                                                                                                                         Kmiecik D., Sellos D., Belaiche D., Sautiere P., Primary structure of the two variants of a sper from the annelid Platynereis dumerili."; Eur. J. Biochem. 150:359-370(1985).

-i- FUNCTION: HISTONES HI ARE NECESSARY FOR THE CONCION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Platynereis dumerilii (Dumeril's clam worm).
Eukaryota; Metazoa; Annelida; Polychaeta; Pa
Phyllodocida; Nereididae; Platynereis.
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InterPro; IPR003216; Linkerhist_N.
Pfam; PF00538; linker_histone; 1.
ProDom; PD000373; Linkerhist_N; 1.
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L; AE00316; AAC75326.1; -..
L; D90858; CAB22026.1; -..
L; D90857; CAB22016.1; -..
L; 250849; -; NOT_ANNOTATED_CDS.
L; AE005459; AAG57399.1; -..
L; AP002551; BAB36577.1; -..
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RESULT 16
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"Leukocystatin, a new class II cystatin caprocelle cells.";

hematopoietic cells.";

J. Biol. Chem. 273:16400-16408(1998).

-i- FUNCTION: INHIBITS PAPAIN AND CAPHEPSIN L BUT WITH AFEINITIES LOWER THAN OTHER CYSTATINS. MAY PLAY A ROLE IN IMMUNE REGULATION THROUGH INHIBITION OF A UNIQUE TARGET IN THE HEMATOPOIETIC SYSTEM.

-i- SUBCELULAR LOCATION: Secreted (Probable).

-i- SUBCELULAR LOCATION: Secreted (Probable).

-i- SIMILARITY: BELONGS TO THE CYSTATIN FAMILY.

-i- SIMILARITY: BELONGS TO THE CYSTATIN FAMILY.

-i- SIMILARITY: BELONGS TO THE CYSTATIN FAMILY.
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15-DEC-1998 (Rel. 37, I
01-MAR-2002 (Rel. 41, I
Cystatin F precursor (I
metastasis-associated p
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MEDLINE=98398157; PubMed=9632704;

Halfon S., Ford J., Foster J., Dowling L., Lucian L., Sterling M.,

Xu Y., Weiss M., Ikeda M., Liggett D., Helms A., Caux C., Lebecque

Hannum C., Menon S., McClanahan T., Gorman D., Zurawski G.;
                                                                                                                                                                                                                                                                                           MGD; MGI:1298217; Cst7.
InterPro; IPR000010; Cystatin.
InterPro; IPR003243; Cystatin_C_M.
Pfam; PF00031; Cystatin; 1.
ProDom; PD001231; Cystatin_C_M; 1.
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Mammalia; Eutheria;
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 PR12_HORVU
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Sciurognathi; Muridae;
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HSSP; P04284; LLL.

R HSSP; P04284; LLL.

R InterPro; IPR001283; SCP.

JR Pfam; PF00188; SCP; 1.

DR PRINTS; PR00837; V5TPXLIKE.

DR SMART; SM00128; SCP; 1.

DR PROSITE; PS01009; SCP_AG5_PR1_SC7_2; 1.

DR PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.

DR PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.

DR PROSITE; PS01010; SCP_AG5_PR1_SC7_1; 1.

DR PROSITE; PS01000; SCP_AG5_PR1_SC7_1; 1.

DR PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.

DR PROSITE; PS01010; SCP_AG5_PR1_SC7_1; 1.

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Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Pathogenesis-related protein PRB1-2
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Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Triticeae; Hordeum.
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RESULT 18
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
BEDLINE-94033324; PubMed-8219079;
MUTAGOV A., Petrasovits L., Davidson A., Scott K.J.;
"A cDNA clone for a pathogenesis-related protein 1 from barley.";
Plant Mol. Biol. 23:439-442(1993).
-1- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS
-1- FUNCTION: PROBABLY INVOLVED IN THAT GROUPS MAMMALIAN SCP/TPX
THAT GROUPS MAMMALIAN SCP/TPX
                       STRAIN=CS7BL/6; TISSUE=Bone marrow; STRAIN=CS7BL/6; PubMed=9148921; Gallo R.L., Kim K.J., Bernfield M., Kozak C.A Merluzzi L., Gennaro R.; "Identification of CRAMP, a cathelin-related processing the combruonic and adult mouse.";
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                                                                                                                                                                       like protein)
CNLP OR CRAMP.
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Pfam; PF00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
SMART; SM00198; SCP; 1.
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PIR; S39474; S39474.
HSSP; P04284; 1CFE.
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           Chem.
          in the embryonic and adult Chem. 272:13088-13093(1997).
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Sciurognathi; Muridae;
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                      adult mouse.
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                                                         C.A.,
                                  antimicrobial peptide
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P48177;
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygil; Neopterygil; Teleostel;
Protacanthopterygil; Salmoniformes; Salm
NCBI_TaxID=8022;
                                          Oncorhynchus mykiss Mitochondrion.
                                                                  NADH-ubiquinone
MTND6 OR ND6.
                                                                                      01-FEB-1996 (Rel. 33, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
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InterPro; IPR001894; Cathelicidin.
Pfam; PF00666; Cathelicidins; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U43409; AAA85888.1; -.
EMBL; Sy4353; CAA64078.1; -.
EMBL; AF035680; AAB88303.1; -.
HSSP; P25230; ILYP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUTTHOR K.M., PITAINO J., GALLO R.L.;
SUBMITTED (DEC-1997) TO THE EMBLYGEBBANK/DDBJ databases
-I- FUNCTION; ACTS AS A POTENT ANTIMICROBIAL PEPTIDE.
-I- TISSUE SPECIFICITY: EXPRESSED IN TESTIS, SPLEEN, STO.
INTESTINE: VERY LOW EXPRESSION FOUND IN HEART, LUNG
MUSCLE, NO EXPRESSION IN BRAIN, KIDNEY OR LIVER.
-I- SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-Bone marrow;
MEDLINE-96326596; PubMed-8706928;
MEDLINE-96326596; PubMed-8706928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This
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                                                                                                                                                                                                                                                                                                                                                                                                         Antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A novel murine cathelin-like FEBS Lett. 391:5-8(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                   PFam; PR00666; Cathelicidins; 1.
ProDom; PD001838; Cathelicidin; 1.
PROSITE; PS00946; CATHELICIDINS_1;
PROSITE; PS00947; CATHELICIDINS_2;
                                                                                                                                                                                           19
                                                                                                                                                                                                      16 LLLLIGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed.
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                                                                                                                                    STANDARD;
                                                                             oxidoreductase
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122
24
173
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SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
L -> M (IN REF. 2).
MISSING (IN REF. 1).
MISSING (IN REF. 1).
                                                                                                                                                                                                                                     0;
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Pred. No. 22;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
CATHELIN-RELATED ANTIMICROBIAL PEPTIDE.
PYPROT.TDONE CARBOXYLIC ACID (BY
                                                      trout) (Salmo
                                                                   e chain 6 (EC 1 )
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                                                                                                                                    PRT;
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           Salmonidae;
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                      Euteleostei
                                 Vertebrata;
                                                      gairdneri)
                                                                            1.6.5.3).
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                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                            Length 173;
           Oncorhynchus
                                                                                                                                                                                                                                                                                             CRC64;
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                                 Euteleostomi;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L29771; AAB03358.1; -.
InterPro; IPR001457; Oxidored_q3.
Pfam; PF00499; oxidored_q3; 1.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 173 AA; 18144 MW; A02134BCC15D0C3F CRC64;
                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protacanthopterygii; Salmoniformes; Salmonidae; Salmo. NCBI_TaxID=8030;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      salar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hurst C.D., Bartlett S.E., Davidson W.S., Bruce "The complete mitochondrial DNA sequence of the salar.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20018174; PubMed=10548724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitochondrion.
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MO1. Evol. 41:942-951(1995).
- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGLVLGL 16
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100.0%; Pr
0;
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Pred. No.
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Atlantic salmon,
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219 LGLGLVL 225

Query Match Best Local S Matches 7

2.5%; Similarity 100.0%; 7; Conservative

0;

Score 7; DB 1; Pred. No. 25; 0; Mismatches

DB 25;

Length 200

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NQOA_PARDE
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Best Local :
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                      Oxidoreductase; I
TRANSMEM 2
TRANSMEM 26
TRANSMEM 51
TRANSMEM 90
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01-APR-1993
 TRANSMEM
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SEQUENCE
                                                                                                                                                                                                                                                       EMBL; U12143; AAD04744.1; -.
EMBL; AF133701; AAF61389.1; -.
INTERPro; IPR001457; Oxidored_q3.
Pfam; PF00499; oxidored_q3; 1.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 173 AA; 18388 MW; 55322B94E972CE17 CRC64;
                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
01-NOV-1995 (Rel. 32, Last annotation 10 (EC 1)
NADH-ubiquinone oxidoreductase chain 10 (EC 1)
dehydrogenase 1, chain 10) (NDH-1, chain 10).
                                                                                    Pfam; PF00499; oxidored_q3;
                                                                                                            EMBL; L02354; AAA25596.1; PIR; F45456; F45456.
                                                                                                                                                                                                                                                                                                                                                       Xu X., Matsuno-Yagi A., Yagi T.;
"DNA sequencing of the seven remaining
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93136200; PubMed=8422400;
                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Paracoccus
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Paracoccus
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                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOOA_PARDE
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                                                                                                                                                                                                                                              OF CHLOROPLASTS OR MITOCHONDRIA.
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Proteobacteria;
                                                                                               IPR001457; Oxidored_q3.
  200 AA;
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                                                                          NAD; Ubiquinone; Transmembrane.
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164
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. 22;
                                                                                                                                                                                                                                                                                                                                             structural genes of the gene NADH-quinone oxidoreductase
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  CRC64;
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HAZO, HUMAN
ACC PHOMAN
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DT 21-JUL
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DE HLA cl
CC CWANDMAN
RN SEQUE
RN ALAWYZIN
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01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
HLA class II histocompatibility antigen, DP al
(HLA-SB alpha chain) (MHC class II DP3-alpha)
HLA-DPA1 OR HLASB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HA2Q_HUMAN
P20036; P019
21-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                          histocompatibility entigen alpha-chain genes.";
Nature 308:327-333(1984).
                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 28-260 FROM N.A.
MEDLINE-84168117; PubMed-6584734;
Auffray C., Lillie J.W., Arnot D.,
Strominger J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-89053719; PubMed-2461352; Young J.A., Lindsay J., Bodmer J.G., Trowsdale J.; Young J.A., Lindsay J., Bodmer J.G., Trowsdale J.; Epitope recognition by a DP alpha chain-specific (DP11.1) is influenced by the interaction between and its polymorphic DP beta chain partner."; Hum. Immunol. 23:37-44(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gustafsson K., Widmark E., Jonsson A.-K., Servenius B. Larhammar D., Rask L., Peterson P.A.; "Class II genes of the human major histocompatibility Evolution of the DP region as deduced from nucleotide the four genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-86041930; PubMed-2997750;
Lawrance S.K., Das H.K., Pan J., Weissman
"The genomic organisation and nucleotide s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids
                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-87250502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133
                                                                                                                                                                              IL; X03100; CAA26887.1; -.
IL; X03100; CAA26887.1; -.
IL; X07487; AAA633220.1; -.
IL; X00457; CAA25143.1; -.
IL; A02209; HLHUSB.
IL; A02313; A29313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGLGLVL
                                                                                                                                             142880;
                     PF00047; 1g; 1.
PF00993; MHC_II_alpha;
; SM00407; IGc1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene.";
                                                                                                                                                              P01903; 2SEB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genes.";
Chem. 262:8778-8786(1987).
                                                                                                                                                                                                                                                                                                                                                                        non-profit institutions as long
      PS00290; IG_MHC; 1
                                                                           IPR003006; Ig_MHC.
IPR003597; Ig_c1.
IPR001003; MHC_II_alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=3036829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13:7515-7528(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Grossberger D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260
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                                                                                                                                                                                                                                                                                                                                                                      as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kappes
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Best Local S
Matches 7
PRINTS; PRO0164; ABC2TRNSPORT.
PROSITE; PS00890; ABC2_MEMBRANE; 1.
POLYSACCHARIDE transport; Transport
TRANSMEM 37 57 POTENTI
TRANSMEM 64 84 POTENTI
TRANSMEM 118 138 POTENTI
TRANSMEM 151 171 POTENTI
TRANSMEM 178 198 POTENTI
TRANSMEM 178 198 POTENTI
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01-NOV-1990
01-NOV-1990
16-OCT-2001
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to licenseelsb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Capsulation in distantly related strains of Haemophilus influenzae type b: genetic drift and gene transfer at the capsulation locus.";
J. Bacteriol. 172:1374-1379(1990).
-i- FUNCTION: MAY FORM AN ATP-DRIVEN CAPSULE POLYSACCHARIDE EXPORT APPARATUS, IN ASSOCIATION WITH THE BEXA, BEXC AND BEXD PROTEINS.
-i- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-90170850; PUBMEd-2137816; Kroll J.S., Moxon E.R.; "Capsulation in a series of the series of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              вхв1
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. ||||||
228 LGLVLGL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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SIGNAL
                                                                                                                                                                                                                                                                                               InterPro; IPR000412; ABC2_transport.
Pfam; PF01061; ABC2_membrane; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-RM 153 / SEROTYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Capsule
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                                                                                                                                                                                                                                                                                                                                                                            EMBL; M33787; AAA24945.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-727;
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(Rel. 16, Last sequence update)
(Rel. 40, Last annotation update)
ysaccharide export inner-membrane |
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   Transport; Transport; Transport Tran
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Pred. No.
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-LINKED (GLCANC. . .) (POTENTIAL).

N-LINKED (GLCANC. . .) (POTENTIAL).

I -> F (IN REF. 4).
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EXTRACELLULAR ALPHA-2.
CONNECTING PEPTIDE.
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DT 01-AUG
DT 01-BEXB.
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between
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STRAIN-EAGAN / SEROTYPE B;
MEDLINE-91186821; PubMed-2082145;
MEDLINE-91186821; PubMed-2082145;
Kroll J.S., Loynds B., Brophy L.N., Moxon E.R.;
"The bex locus in encapsulated Haemophilus influenzae: a chr. region involved in capsule polysaccharide export.";
mol. Microbiol. 4:1853-1862(1990).
-I- FUNCTION: MAY FORM AN ATP-DRIVEN CAPSULE POLYSACCHARIDE APPARATUS, IN ASSOCIATION WITH THE BEXA, BEXC AND BEXD APPARATUS, IN ASSOCIATION WITH THE BEXA, BEXC AND BEXD APPARATUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P22235;
01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000412; ABC2_transport.
Pfam; PF01061; ABC2_membrane; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Capsule
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                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                         Polysaccharide
                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                           PRINTS;
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                 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
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                                                                               h 2.5%;
Similarity 100.0%;
7; Conservative
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; PS00890; ABC2_MEMBRANE; 1
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37 57
64 84
18 138
51 171
78 198
35 255
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                                                                             Score 7; DB 1;
b; Pred. No. 32;
0; Mismatches
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RESULT 26
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Q48215; O05081;
16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
01-MAR-2002 (Rel. 4
Putative glycosyl t
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                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There as use by non-profit institutions as long as is modified and this statement is not removed. Us
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=RD / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
LEP4_SYNY3
P72640;
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                                                                                                                                                                                              Local Similarity nes 7; Conserv
                                                                                                                                                       49 GNGMVSR 55
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transferase HI1695 (EC 2.-.-).
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Pred. No.
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RESULT
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HOFD OR SLR1120.
Synechocystis sp. (strain
Bacteria; Cyanobacteria; C
NCBI_TaxID=1148;
                                                                   01-JUL-1993
01-JUL-1993
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               enzymes (EC 3.4. OUTO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Type 4 prepilin-like proteins leader peptide processing enzyme [Includes: Leader peptidase (EC 3.4.99.-) (Prepilin peptidase);
methyltransferase (EC 2.1.1.-)}.
  Erwinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000045;
Pfam; PF01478; Peptic
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                                                                                                                                                                                                                                                                                                                                                                                                                      Methyltransferase;
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                           ymes secretion
3.4.99.-) (Pro
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                     JL-193 (Rel. 26, Created)
JL-193 (Rel. 26, Last sequence update)
JL-1993 (Rel. 26, Last sequence update)
CT-2001 (Rel. 40, Last annotation update)
4 prepilin-like proteins leader peptide processing
5 prepilin-like protein outo) [Includes: Leader peptides]
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                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane;
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dase_C20; 1.
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Chroococcales;
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                            N-methyltransferase (EC
                                                                                                                                                                                                                                                                  DB 1
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mura T.,
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                                                        enzyme (Pectic
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TRANSMEM 106
TRANSMEM 128
TRANSMEM 153
TRANSMEM 176
TRANSMEM 216
TRANSMEM 259
SEQUENCE 283 AA;
                                                                                                     01-NOV-1997 (
16-OCT-2001 (
Hypothetical
MJ0635.
  STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE-96337999; PubMed-868087, Zhou
Bult C.J., White O., Olsen G.J., Zhou
Sutton G.G., Blake J.A., FitzGerald L
                                                                                                                                               Q58052;
01-NOV-1997
                                                                                                                                                                            METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. The use by non-profit institutions as low modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genes from other Gram-negative bacteria.";
J. Bacteriol. 174:7385-7397(1992).
-i- FUNCTION: CLEAVES TYPE-4 FIMBRIAL LEADER SEQUENCE AND
THE N-TERMINAL (GENERALLY PHE) RESIDUE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L02214; AA
PIR; C47755; C47
MEROPS; A24.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This
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"Analysis of eight out genes in a secretion by Erwinia chrysanthemi:
                                                             Methanococcus.
NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00864; PREPILI Multifunctional enzyme;
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STRAIN-EC16
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Pectobacterium
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SIMILARITY: BELONGS TO PEPTIDASE FAMILY A24; ALSO
III LEADER PEPTIDASE FAMILY.
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                                                                                 Euryarchaeota;
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nilarity 100.0%;
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33 POTENTIAL.
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rald L.M.,
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01-APR-1990
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                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                        EMBL; J02058; -; NOT_ANNOTATED_CDS.
INTERPRO; IPRO00211; Gemini_BL.
Pfam; PE00845; Gemini_BL1; 1.
SEQUENCE 298 AA; 33773 MW; D1E3
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cassava latent virus (strain West Kenyan 844).
Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BL1 protein
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                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO GEMINIVIRUSES BL1 PROTEIN FAMILY.
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Pfam; PF00845; Gemini_BL1; 1.
SEQUENCE 298 AA; 33648 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acids Res. 18:197-198(1990).
-!- SIMILARITY: BELONGS TO GEMINIVIRUSES BL1 PROTEIN FAMILY.
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                                                                                                                                                                                                                                                                      sp_organelle:*
sp_phage:*
sp_plant:*
                                                                                                                                                                                                               sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
  sp_fungi:*
sp_human:*
sp_invertebrate:*
                                                                                                                                                                                                                                                                                                sp_mhc:*
                                                                                                                                                                                                                                                       sp_rodent:*
sp_virus:*
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                                                                                                                                       Length
109
151
162
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0920X4
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     O02764 oryctolagus
O920t6 mus musculu
O920x4 mus spicile
Q9uf74 homo sapien
O9cwe9 mus musculu
O51707 borrelia bu
O9nfu2 plasmodium
O9h7a9 homo sapien
O9h8m8 rhizobium 1
O9nfu4 plasmodium
O9d5a9 mus musculu
O20614 caenorhabdi
O31625 brachydanio
O31150 mus musculu
                                                                                                                                       Description
Q9qwv1 mus musculu
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473 164 473 164 476 166 476 166 576 11 621 4 852 4 1031 10 47 10 47 10 100 12 100 12 100 12 110 113 2 1113 2 1114 13 115 13 115 13 116 110 117 13 16 118 13 119 16 119 19 19	264 4 282 4 306 2 315 16 329 10 432 16
1 090776 6 05395 6 050017 7 091177 099277 099267 000279 099566 0 065500 0 095596 0 095674 0 091188	
OSC276 mus musculu OSC295 mycobacteri OSO017 mycoba	lero lomo stap stap pop pop

## ALIGNMENTS

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RESULT
Q920X4
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Best Local S
Matches 9
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Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000636; Cation_chan_non_lig.
InterPro; IPR002111; Cat_channel_TrpL.
InterPro; IPR0021024; LH2.
InterPro; IPR000203; PKD_cys_rich.
InterPro; IPR002859; REJ.
Pfam; PF00520; ion_trans; 1.
Pfam; PF01477; PLAT; 1.
Pfam; PF012010; REJ; 1.
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Q9Z0T6;
Q9Z0T6;
01-MAY-1999
01-DEC-2001
POLYCYSTIC K
                                                                                                                                                                                                                01-DEC-2001
01-DEC-2001
01-DEC-2001
                                                                                           Mus spicilegus (Steppe mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDILINE-99138702; PubMed-9949214;

Hughes J., Ward C.J., Aspinwall R., Butler R., Harris P.

"Identification of a human homologue of the sea urchin
egg jelly: a polycystic kidney disease-like protein.";

Hum. Mol. Genet. 8:543-549(1999).

EMBL; AF116459; AAD18022.1;

MGD: MGI:1338786; Pkdrej.
                      STRAIN-ZBN;
Liu Y., Kit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
MCBI_TaxID=10090;
                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                CRAMP
                                                                                                                                                                                                CATHELICIDIN
                                                                                                                                                                                                                                                                           Q920X4;
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      "Conspicuous
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                    Kitano
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9; Conserv
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9 (TrEMBLrel. 10, Last sequence update)
1 (TrEMBLrel. 19, Last annotation update)
KIDNEY DISEASE AND RECEPTOR FOR EGG JELLY
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l (TrEMBLrel. 1
l (TrEMBLrel. 1
(N (FRAGMENT).
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    Differences
                      Τ.,
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LH2;
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T., Shiroishi T., Mori
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Last sequence update)
Last annotation updat
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Pred. No.
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Pred. No.
                                                                                                                   Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Sciurognathi; Muridae;
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1.9e-08;
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  . K., Saitou
21 Nuclear (
                                                                                                                                       Euteleostomi;
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                                                                                                                     Murinae;
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  u N.;
Genes
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Best Local S
Matches 8
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Best Local S
Matches 8
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Submitted (FEB-2000) to the EMBL,
EMBL; AB039073; BAB68597.1; -.
NON_TER 109 109
SEQUENCE 109 AA; 12230 MW; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                       09CWE9;
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
2410141K03RIK PROTEIN.
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Q9UF74;
01-MAY-2000
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01-MAY-2000
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=EMBRYONIC
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Poustka A., Klein M., Mewes
Submitted (DEC-1999) to the
EMBL; AL133575; CAB63722.1;
Hypothetical protein.
NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DKFZP434N1535
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8; Conserv
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8; Conser
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11 16.6 KDA PR
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BLrel. 13, Last sequence up
BLrel. 13, Last annotation
KDA PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                        Chordata;
Rodentia;
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17,
19,
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Last sequence up
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Pred. No. 6.7
0; Mismatches
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Pred.
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Sciurognathi; Muridae;
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                                                                                                     Complete SEQUENCE
                                                                                                                                                                                               "Genomic sequence of a Lyme burgdorferi.";
                                                                                                                                                                                                                                  Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwil Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O51707 PRELIMINARY; PRT; 162 AA. 051707; 01-JUN-1998 (TrEMBLrel. 06, Created) 01-JUN-1998 (TrEMBLrel. 06, Last sequence up 01-JUN-2001 (TrEMBLrel. 17, Last annotation COLICIN V PRODUCTION PROTEIN, PUTATIVE.
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-ATCC 35210 / B31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AK010803; BAB27191.1; -.
MGD; MGT:1915216; 2410141K03Rik.
InterPro; IPR001878; Znf_CCHC.
Pfam; PF00098; Zf-CCHC; 1.
SMART; SM00343; Znf_CZHC; 1.
                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98065943; PubMed=9403685;
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Bacteria; Spirochaetales; S
                                                                                                                                InterPro; IPR003825; Colic
Pfam; PF02674; Colicin_V;
                                                                                                                                                             TIGR; BB0766;
                                                                                                                                                                Nature 390:580-586(1997).
EMBL; AE001176; AAC67114.1;
TIGR; BB0766; -.
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221 LGLVLGLL
                                            Local
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8; Conserv
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8; Conser
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162 AA;
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                                Conservative
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Spirochaetaceae; Borrelia
                             Score 8; DB 1
s; Pred. No. 9.4
0; Mismatches
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Pred. No
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                                                         Length 162;
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SEQUENCE FROM N.A.

KAWAKAMI T., Noguchi S., Itoh T., Shige
Nakajima Y., Mizuno T., Morinaga M., Ta
Yamada K., Fujii Y., Ozaki K., Hirao M.
Obayashi M., Nishi T., Shibahara T., Ta
ISOgai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBan
EMBL; AKO24757; BAB14988.1; --
SEQUENCE 191 AA; 20917 MW; COEBB496
                                                                                                                                                                                                                                                                                                                                                                                                                   Q9H7A9
Q9H7A9;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created
01-MAR-2001 (TrEMBLrel. 16, Last se
01-MAR-2001 (TrEMBLrel. 16, Last an
CDNA: FLJ21104 FIS, CLONE CAS04958.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=3D7A;
MEDLINE=20520959; PubMed=11071280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIANO P., Silvestrini F., Roca L.;
"Structure and polymorphism of the upstream region of the pfg 27/25 gene, transcriptionally regulated in gametocytogenesis of Plasmodium falciparum.";
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Eukaryota; Alveolata;
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                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mol. Biochem. Parasitol. 110:247-257(2000). EMBL; AJ271108; CAB93664.1; -.
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(TrEMBLrel. 15, Last sequence
(TrEMBLrel. 19, Last annotati
L 21.7 KDA PROTEIN (FRAGMENT).
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rini F., Roca L.;
                                                                                                                                                                                                                                                                          Chordata;
Primates;
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                                                EMBL/GenBank/DDBJ
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    C0EBB49678F36E0B CRC64;
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                                                                                                              Shigeta K., Senba T., Matsumura
M., Tanigami A., Fujiwara T., Onc
rao M., Ohmori Y., Ota T., Suzuki
T., Tanaka T., Nakamura Y.,
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence
01-DEC-2001 (TrEMBLrel. 19, Last annotati
HYPOTBETICAL 23.8 KDA PROTEIN (FRAGMENT).
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MEDLINE-21082930; PubMed-11214968;
MEDLINE-21082930; PubMed-11214968;
Mannabe A., Nakamura Y., Sato S., Asamizu E., Kato T., Sasa Matanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura Mitanabe A., Kiyokawa C., Kohara M., Matsumoto M., Matsuno Mochizuki Y., Nakeyama S., Nakazaki N., Shimpo S., Sugimot Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                       Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                    "Repetitive sequences upstream of the polymorphism in laboratory and natural
                                                                                                           Sallicandro P., Paglia M.G., Ha
Gentile M., Mulaa F., Alano P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome structure of Mesorhizobium loti."; DNA Res. 7:331-338(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Phyllobacteriaceae; Mesorhizobium.
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                                                                                                                                  MEDLINE=20520959; PubMed=11071280;
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Mismatches
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Sugimoto M
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                                                                                                                            SEQUENCE
                                                                                                                                         PRINTS; PR00794; RIBONUCLEASE. ProDom; PD000535; RNaseA; 1. SMART; SM00092; RNASe_Pc; 1.
                                                                                                                                                                                                                                                                             Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L. Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-TESTIS;
MEDLINE-21085660; PubMed-112178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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01-JUN-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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Q9D5A9;
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50 VAAILGLG
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llarity 100.0%;
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21
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AA; 23407
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17,
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Q31625;
Q31625;
Q1-NOV-1996 (TrEMBLrel. 01, C;
Q1-NOV-1996 (TrEMBLrel. 19, L;
Q1-DEC-2001 (TrEMBLrel. 19, L;
MHC CLASS II ALPHA CHAIN.
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDILINE-94011091; PubMed-8406613;

MIDILINE-94011091; PubMed-8406613;

Sultmann H., Mayer W.E., Figueroa F., O'Huigin C., Klein
"Zebrafish Mhc class II alpha chain-encoding genes: polyn
"Zebrafish machion.":
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Q20614;
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                                                             MHC.
SEQUENCE
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Science 282:2012-2018(1998).
EMBL; 266520; CAA91386.1; -.
SEQUENCE 215 AA; 24861 MW;
                                                                                                                                                                                                                                                                                     expression, and function.";
Immunogenetics 38:408-420(1993).
EMBL; L19450; AAA16369.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Verti
Actinopterygii; Neopterygii; Teleostei; Eute
Cypriniformes; Cyprinidae; Danio.
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Rhabditidae; Pelode
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01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
F49E12.7 PROTEIN.
                                                                                                                         Pfam; PF00047; ig; 1.
Pfam; PF00993; MHC_II_alpha;
SMART; SM00407; IGc1; 1.
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HSSP; P01888; 1BMG.
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IPR003006; Ig_MHC.
IPR001003; MHC_II_alpha.
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                                                                                                    IG_MHC; UNKNOWN_1
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red. No. 12;
Mismatches
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DR InterPro; IPRO03006; Ig_MHC.

DR InterPro; IPRO01003; MHC_II_alpha.

Pfam; PF00047; Ig; 1.

Pfam; PF00993; MHC_II_alpha; 1.

R SMART; SM00407; IGcl; 1.

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SEQUENCE 236 ...
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Matches 8; Conser
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Q31150;
01-NOV-1996 (TrEMBLrel. C
01-NOV-1996 (TrEMBLrel. C
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01-DEC-2001 (TREMBLREL. CHAIN
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Q31359;
01-NOV-1996 (TrEMBLrel. (
01-NOV-1996 (TrEMBLrel. (
01-DEC-2001 (TrEMBLrel. 1
                              EMBL;
HSSP;
MGD; M
                                                                                                   Karlsson L., Peterson P.A.;
"The alpha chain gene of H-20 has
"The Med. 176:477-483(1992).
"The Alpha Chain gene of H-20 has
                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-B10.M; TISSUE-SPLEEN;
MEDLINE-92364550; PubMed-1354242;
Karlsson L., Peterson P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brachydanio rerio (Zebrafish) (Zebra dai
Eukaryota; Metazoa; Chordata; Craniata;
Eukaryota; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
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EMBL; L19445; AAA16367.1; •
HSSP; P01888; 1BMG.
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MEDLINE-94011091; PubMed-8406613;

Sultmann H., Mayer W.E., Figueroa F., O'Huigin C., I
"Zebrafish MHC class II alpha chain-encoding genes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MHC CLASS II ALPHA CHAIN.
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                              MGI:95924;
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                                                      M95514; AAB46387.1;
P01903; 1A6A.
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8; Conserv
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1 (TrEMBLrel. 1
II ALPHA CHAIN
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                                 H2-0a.
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    26136 MW; 3780A1609ACBE285 CRC64;
                                                                                                                                                                                                                                                                                                                                              Chordata;
Rodentia;
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Sciurognathi; Muridae;
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Euteleostei;
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; Ostariophysi;
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                                                                                                                                                                                                                                                                                 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh.M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Havashizaki Y., Soshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Best Local S
Matches 8
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Q9QWV1;
01-MAY-2000
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SIGNAL
                                                                                                                Nature 409:685-690(2001).
EMBL; AF100956; AAC69906.1;
EMBL; AK020594; BAB32142.1;
HSSP; P01903; 1A6A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Sequence region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-C57BL/6J; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rowen L., Qin S., Madan A., Loretz C., James R., Dors M., Mix Hall J., Lasky S., Hood L.;
"Sequence of the mouse major histocomaptibility locus class II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Rodentla;
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
H2-O ALPHA (HISTOCOMPATIBILITY 2, O REGION ALPHA LOCUS).
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Pfam; PF00993; MHC_II_alpha; 1.
SMART; SM00407; IGC1; 1.
                                                                                                                                                                                                                                       "Functional annotation of a full-length mouse cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-C57BL/6J; TISSUE-URINARY BLADDER; MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-129SVJ;
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                                                                                                                                                                                                                                                                        layashizaki Y.;
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                                                                                     MGI:95924; H2-Oa.
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IPR003597; Ig_c1.
IPR003006; Ig_MHC.
IPR001003; MHC_II_alpha.
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IPR001003; MHC_II_alpha.
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250 N
28182 MW;
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MHC CLASS II ALPHA CHAIN.
; C20A397B2EFA2004 CRC64;
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Q1-OCT-2000 (TrEMBLrel. 15,
Q1-OCT-2000 (TrEMBLrel. 15,
Q1-DEC-2001 (TrEMBLrel. 19,
RDG ANTIGEN (HYPOTHETICAL.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9X647;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
HYPOTHETICAL 28.2 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 1.
Pfam; PF00993; MHC_II.alpha; 1.
SMART; SM00407; IGC1; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SEQUENCE 250 AA; 28166 MW; 98BCF2F8926076A1 CRC64;
                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01569; PAP2;
Hypothetical protein.
SEQUENCE 264 AA; 2
                                                                                                                                                                                                                                                                                                                                                                      Aguilar A., Merino S., Nogueras M.M., Regue M., Tomas J.M.;
"Two genes from the capsule of Aeromonas hydrophila (serogroup 0:34)
confer serum resistance to Escherichia coli K-12 strains.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF131869; AAD34732.1; -.
InterPro; IPR000326; PA_PFPPase.
Pfam; PF01569; PAP2; 1.
human gene
         Auffray C., Ansorge
Lehrach H., Poustka
"The European IMAGE
                                                                                                                                                                                                          Q9NPF0
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                                                            Submitted
                                                                     SEQUENCE FROM N.A. Carim L., Estivill
                                                                                                                                             DKFZP56401762
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                                         SEQUENCE FROM
                                                                                                     NCBI_TaxID=9606;
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Proteobacteria; gamma
                                                            (JUL-2000)
transcripts.";
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                    Ballabio A.,
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9.0 KDA PROTEIN).
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Pred. No. 14;
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Pred.
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Q9FDT4;
Q9FDT4;
01-MAR-2001
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EXFOLIATIVE
SHETA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Choi Y.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted [3]
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"Cloning of the gene coding for St. toxin A and its expression in Esch J. Bacteriol. 182:4101-4103(2000).
EMBL; AB036768; BAB08178.1; -.
SEQUENCE 306 AA; 34379 MW; 60B
                                                                                                      Staphylococcus hyicus.
Bacteria; Firmicutes; Bacillus/Staphylococcus
                                                                                                                                                                                                                                                                                                          Glycoprotein
SEQUENCE 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Identification of a human follicular den stimulates germinal center B cell growth. J. Exp. Med. 191:1077-1084(2000).
                                                   STRAIN-P-1;
MEDLINE-20327593; PubMed-10869091;
MEDLINE-20327593; PubMed-10869091;
                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002172; LDL_recept_A.
Pfam; PF00057; ldl_recept_a; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=BRAIN;
                                           Watanabe T., Sato H., I
Aizawa C., Danbara H.,
                                                                              SEQUENCE
                                                                                               NCBI_TaxID=1284;
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
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TISSUE=KIDNEY ADENOCARCINOMA;
Strausberg R.;
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AL136652; CAB66587.1;
BC000668; AAH00668.1;
BC007083; AAH07083.1;
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AL365455; CAB9
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llarity 100.0%;
Conservative
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                                           Sato H., Hatakeyama Y
anbara H., Maehara N.;
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Kovacic S., Long
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60B7EDF3677ACDDF
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Q43324;
01-NOV-1996
01-NOV-1996
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                                                            Populus x canadensis.
Eukaryota; Viridiplantae; Streptophyti
Spermatophyta; Magnoliophyta; eudicot;
eurosids I; Malpighiales; Salicaceae;
MCBI_TaxID=3690;
                                                                                                                                                                                                                                                                                                                                                                        Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-O., Ito T., Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., S., Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.; Whole genome sequencing of meticillin-resistant Staphylococcu aureus "37:1225-1240(2001).
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01-NOV-1996 (TremBLrel.
01-DEC-2001 (TremBLrel.
MAJOR STORAGE PROTEIN.
           "Seasonal changes
                                                                                                                                                                                                                                                                                                                              Hypothetical protein; Complete SEQUENCE 315 AA; 35236 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus/Staphylococcus group;
NCBI_TaxID=158879, 158878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus (strain N315), Staphylococcus aureus (strain Mu50).
                    SEQUENCE FROM N.A. MEDLINE=92003681; FC Clausen S., Apel K.
                                                                                                                                                                                                                                                                                                                                                    EMBL; AP003132; BAB42268.1; EMBL; AP003361; BAB57335.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Cerdeno A.M.,
Submitted (JUN
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01-MAR-2001 (TrembLrel.
01-OCT-2001 (TrembLrel.
HYPOTHETICAL PROTEIN PAGE
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Submitted (JUN-2001)
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE INTEGRAL MEMBRANE PROTEIN.
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EMBL; S59422; AAB20113.2; -.
SEQUENCE 329 AA; 36055 MW; 875
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Kinashi H., Hopwood D.A.;
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                                                                  Paeudomonas
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EMBL; AL592126; CAC42144.1; -.
SEQUENCE 432 AA; 43516 MW; DC22211287
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PROTEIN PA4323.
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e EMBL/GenBank/DDBJ databases.
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                                                                                                subdivision; Pseudomonadaceae;
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RA Arakawa T., Hara A., Fukunishi Y., Konnoo H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
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RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashina J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
RT., Randaria M., Rodriguez M., Kawaji H., Kohtsuki S.,
RT., Randaria M., Rodriguez M., Kawaji H., Kohtsuki S.,
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5730589L02RIK PROTEIN.
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InterPro; IPR002035; vWFA.
Pfam; PF01882; DUF88; 1.
SMART; SM00327; VWA; 1.
Hypothetical protein; Complete proteome.
Hypothetical protein; Complete proteome.
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5730589L02RIK.
Mus musculus (Mouse).
Mus musculus (Motazoa; Chordata; (Motazoa; Rodentia; Motazoa; Rodentia;
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EMBL; AE004848; AAG07711.1; -
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STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; PubMed-
                  "Functional annotation of a full-length Nature 409:685-690(2001).
EMBL; AK019981; BAB31950.1; -.
MGD; MGI:1924832; 5730589L02Rik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-EMBRYO;
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Mammalia; Eutheria;
NCBI_TaxID=10090;
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CE6F8E93C3D01C4F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
I Nature 393:537-544(1998).
R EMBL; 293777: CAB07836.1; -.
R HSSP; P08659; ILCI:
R TINESTC; IPR000873; AMP-bind.
R InterPro; IPR000873; AMP-bind.
R InterPro; IPR003015; HHH.Myc.
R Pfam; PF00501; AMP-binding; 1.
R PROSITE: PS00455; AMPBINDING.
R PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
R PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
SEQUENCE 473 AA; 49520 MW; 39EECZB0D02BAD3D CRC64;
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01-JUL-1997
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Q50017;
Q1-NOV-1996
01-NOV-1996
01-DEC-2001
XCLC (ACYL-CO
XCLC OR ML10:
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 SEQUENCE
                                   NCBI_TaxID=1769;
                                                                      Bacteria; Firmicutes;
                                                                                         Mycobacterium leprae.
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OR ML1051.
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                                                                      Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                     DB 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24;
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                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                               Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                     Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Holroyd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Harris
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Best Loc
Matches
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InterPro; IPRO00873; AMP-bind
InterPro; IPRO03015; HLH_Myc.
Pfam; PF00501; AMP-binding; 1
PRINTS; PRO0154; AMPBINDING.
PROSITE; PS00455; AMP_BINDING
PROSITE; PS00038; HELIX_LOOP_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  097097
097097;
01-0CT-2001
01-0CT-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-21128732; PubMed=11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Wheeler P.R., Basham D., Brown D., Chillingworth T., Connor R.,
Mungall K., Basham D., Brown D., Chillingworth T., Fraser A., Hamlin N.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith D.R., KUDLL.
                                                                                                                                       Pettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Massive gene decay in the 1
Nature 409:1007-1011(2001).
EMBL; U15181; AAA62961.1; -.
EMBL; AL583920; CAC31432.1;
                                              Science 293:498-506(2001).
EMBL; AE007431; AAK75426.1;
TIGR; SP1328; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Squares S.,
Barrell B.G.
                                                                                                                                                                                                                                                                                                         STRAIN-TIGR4
                                                                                                                                                                                                                                                                                                                                                                            Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SODIUM: SOLUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P08659;
                                                                                                      "Complete genome sequence of pneumoniae.";
                                                                                                                                                                                                                                                                                       MEDLINE=21357209; PubMed=11463916;
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1313;
                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes;
                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    222 GLVLGLLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLVLGLLG
                  PF00474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteome.
00474; SSF;
PS00456; N
                                   IPR001734;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TremBLrel. 18, Created)
(TremBLrel. 18, Last sequence update)
(TremBLrel. 19, Last annotation updat
TE SYMPORTER FAMILY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1LCI.
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 NA_SOLUT_SYMP_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMP_BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HLH_Myc.
binding; 1.
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                                   Na_solut_symport.
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                                                                                                                                                                                                                                                                                                                                                                                             group; Streptococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 476;
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                                                                                                                            Streptococcus
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RESULUTION OF THE PROPERTY OF 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RA Kawai J. Shinagawa A. Shibata K. Yoshino M. Itoh M., Ishii Y.,
RA Alawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kadota K., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninol P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Lee N. H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N. H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N. H.,
RA Wordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Haysshtzaki Y.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 8
                                                       Query Match
Best Local
                             Matches
                                                                                                                                                                                                    MGD; MGI:1926230; Treh.
InterPro; IPR001661; Trehalase.
Pfam; PF01204; Trehalase; 1.
PRINTS; PR00744; GLHYDRLASS37.
PROSITE; PS00927; TREHALASE1; 1.
PROSITE; PS00928; TREHALASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
Complete
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                   Hayashizaki Y.;
"Functional annotation of a full-length mouse Nature 409:685-690(2001).
EMBL; AF136944; AAF61430.1; -.
EMBL; AK008912; BAB25963.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TREHALASE (EC 3.2.1.28 TREH OR 2210412M19RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TREHALASE (EC 3.2.1.28) (2210412M19RIK PROTEIN).
                                                                                                                                                         Hydrolase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-1999)
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Kurimoto M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-DDY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21085660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9JLT2;
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nes 8; Conser
                                                     Local
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                                                       Similarity
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                                                                                                                                                       Glycosidase.
576 AA; 65401 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=INTESTINAL MUCOSA;
do N., Ariyasu H., Yanai Y.,
                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-STOMACH;
; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NA_SOLUT_SYMP_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55768
                                                     2.9%;
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                             <u>.</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ databases
                                                     Score 8;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 8;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                         53CDA6A10511520E CRC64;
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                             Mismatches
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5. 25;
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                                                       28;
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                                                                            Length 576
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A Nagase T., Kikuno R., Ishikawa K., Hirosawa M., Ohara O.;
A Nagase T., Kikuno R., Ishikawa K., Hirosawa M., Ohara O.;
T "Prediction of the coding sequences of unidentified human
genes.XVII.The complete sequences of 100 new cDNA clones fron
T which code for large proteins in vitro.";
L DNA Res. 7:143-150(2000)
L DNA Res. 7:143-150(2000)
R EMBL; AB040897; BAA95988.1; -.
R InterPro; IPR003877; SPRY.
R InterPro; IPR003878; SPRY_domain.
R InterPro; IPR003878; SPRY_domain.
R InterPro; IPR003878; SPRY_domain.
R SMARR; SM00449; SPRY; 1.
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2 SEQUENCE 621 AA; 67385 MW; DBC285CDB9CFD40C CRC64;
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01-OCT-2000
01-OCT-2000
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                     InterPro; IPR000538; Link.
InterPro; IPR000436; Sushi_SCR_CCP
Pfam; PF00084; sushi; 1.
smart; Sm00032; CCP; 1.
                                                                                                                                                 "prediction of the coding sequences of The complete sequences of 100 new cDNA code for large proteins in vitro."; DNA Res. 5:31-39(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-AUG-1998 (TREMBLIGE). 07,
01-JUN-2001 (TREMBLIGE). 17,
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HOmo sapiens (Human).
Homo sapiens (Human).
'arvota; Metazoa; Chordata;
'theria; Primates;
SMART; SM00445; LINK;
                                                                                                                                                                                                                                                           Ohara O.
                                                                                                                                                                                                                                                                              Nagase T., Ishikawa
                                                                                                                                                                                                                                                                                                                                   TISSUE-BRAIN;
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                                                                                                                            BAA25453.1; -.
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wa K., Miyajima
                                                                                                                                                                                                                                                                                                                                                                                                                                     Primates;
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FT NON_TER 1 1 1 SQ SEQUENCE 768 AA; 82680 MW; B97A932B44883536 CRC64;			
Ouery Match 2.9%; Score 8; DB 4; Length 768; Best Local Similarity 100.0%; Pred. No. 36; Matches 8; Conservative 0; Mismatches 0; Indels	0; Gaps	0;	
Qy 14 AALLLIGL 21          Db 161 AALLLIGL 168			
Search completed: June 18, 2002, 14:33:01 Job time: 214 sec			

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Run on:

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US-08-465-360C-8
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US-08-476-347-17
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US-08-795-46B-51
US-08-795-46B-51
US-08-94-574-7
US-08-94-574-7
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Query Match
Best Local Similarity
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Result

50	49	48	47	46	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
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Sequence 10, Appl	Sequence 6, Appli	Sequence 2, Appli	Sequence 5, Appli	Sequence 52, Appl	Sequence 3, Appli	12,		Sequence 12, Appl	Sequence 111, App	•	Sequence 111, App	5	Sequence 6, Appli	Sequence 1, Appli			Sequence 34, Appl	Sequence 4, Appli	Sequence 110, App	110,	Sequence 15, Appl	-

## ALIGNMENTS

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; TYPE: amino a
; TOPOLOGY: lin
; MOLECULE TYPE:
US-08-147-784-2
                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.25

SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/08/147,784

FILING DATE: 03-NOV-1993

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Smith, Willaim M

REGISTRATION NUMBER: 05490A-220

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Godfrey, Wayne
APPLICANT: Buck, David
APPLICANT: Engleman, Edgar G.
TITLE OF INVENTION: RECEPTOR ON THE SURFACE OF ACTIVATED
TITLE OF INVENTION: CD4+ T-CELLS: ACT-4
NUMBER OF SEQUENCES: 2
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CITY: Palo Alto
STATE: California
COUNTRY: US
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100.0%;
Score 277; DB 2;
Pred. No. 1.4e-260;
                       Length 277;
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US-08-195-967-2
; Sequence 2, Application US/08195967
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                                                  Query Match
Best Local S
Matches 277
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                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/195,967
FILLING DATE: 10-FEB-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 05490A-230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                              TELEPHONE: (415) 326-24 TELEFAX: (415) 326-2422 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Godfrey, Wayne
APPLICANT: Engleman, Edgar G.
TITLE OF INVENTION: LIGAND (ACT-4-L) TO
TITLE OF INVENTION: CD4+ T-CELLS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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CITY: Palo Alto
STATE: Callforn
                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
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                                                   Local Similarity
les 277; Conserv
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RRDQRLPPDAHKPPGGGSFRTPIQEEQADAHSTLAKI 277
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                                                Score 277; DB 4;
pred. No. 1.4e-260;
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US-09-006-353A-12
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Matches 277
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Patent No. 6
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                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A
REGISTRATION NUMBER: 36,37
                                                                                                                                                                                                                                                              TELEFAX: (301) 309-85: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
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CCITY: RC
STATE: M
COUNTRY:
COUNTRY:
ZIP: 208
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277;
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                                                                                                                  Similarity
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER
APPLICANT: GENTZ, REINER
APPLICANT: RUBEN, STEVEN
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR
RUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
TOTAL TITLE OF THE CONTENT O
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NTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDSYK 120
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Pred. No. 1.4e-260;
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GENERAL INFORMATION:
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                                                                                                                                                                             Matches
                                                                                                                                                                                                              Query Match
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/147,
FILING DATE: 03-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: SMith, Williaim M
REGISTRATION NUMBER: 30,223
REGISTRATION NUMBER: 0.549
                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 326-24 INFORMATION FOR SEQ ID NO:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Engleman, Edgar G.
TITLE OF INVENTION: RECEPTOR ON THE SURFACE OF ACTIVATED
TITLE OF INVENTION: CD4+ T-CELLS: ACT-4
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
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                                                                                                                                                                                                                                                                                          TYPE: amino acid TOPOLOGY: linear
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FILING DATE: 06-JUN-1995
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                                                              NTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDSYK 120
                                                                                                             MCVGARRLGRGPCAALLLLGLGLSTVTGLHCVGDTYPSNDRCCHECRPGNGMVSRCSRSQ
             PGVDCAPCPPGHFSPGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPATQPQETQ
                                               NTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDSYK 120
1 Similarity
277; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                          protein
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, 326-2422
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                                                                                                                                                                        Score 277; DB 4; Pred. No. 1.4e-260;
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                                                                                                                                                                                                        Length 277;
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RESULT 6
US-08-050-319B-44
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Matches
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                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                       TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                           ID NO:
...ACTERISTICS:
56 amino acids
rrpE: amino acid
STRANDEDNESS: s1'
TOPOLOGY: 1'
OLECULF
166
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Coruzzi, Laura A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 30-MAY-1997 CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: TITLE OF INVENTION:
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STATE:
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                                                      NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 00
                                                                                                               Local Similarity 100 es 56; Conservative
                                                                                                                                                                                                                                                                                                                    TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Pennie & Edmonds LLP STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RRDQRLPPDAHKPPGGGSFRTPIQEEQADAHSTLAKI 277
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Takasaki, Wataru
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100.0%; PI
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ANALOGUES DESIGNED FROM BINDING SITES
NECROSIS FACTOR RECEPTOR SUPERFAMILY A
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                                                                                                               Score 56; DB; Pred. No. 4.1
0; Mismatches
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                                                                                                               4.1e-47;
hes 0;
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Sequence

Application US/08050319B

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                 APPLICANT: M.Feldmann, P.W.
APPLICANT: M.J.C. Turner, F
TITLE OF INVENTION: Modifie
TITLE OF INVENTION: Necrosi
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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NAME: Robbins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 327-3231 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seneral INFORMATION:
                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: Patentin Release #1.0.
               SOFTWARE: PatentIn Release #1.0, version #1.25 CURRENT APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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APPLICANT: M.J.C. Turner, F.M. Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Recepton
NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed & Robbins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS: single
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APPLICATION NUMBER:
                                                                                                                                             COUNTRY:
                                                                                                                                                              CITY: Palo Alto
STATE: California
                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 4.3%; Score 12; DB Local Similarity 100.0%; Pred. No. 0.0 on 12; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/050,319B FILING DATE: 10-May-1993
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California
                                                                                                                                                                                                     635 Bryant Street
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US/08/465,982
                                                                                                                                                                                                                                                                                                                                 P.W.
                                                                                                                                                                                                                                                                                                            W. Gray,
F.M Brennan
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8,
                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, v
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,560C
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR., GERLAD M.
REGISTRATION NUMBER: 28,977
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO:
                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Robbins, Roberta L.
REGISTON NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 51'
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE TITLE OF INVENTION: ANTIGEN NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: NAGATA, Shigekazu
APPLICANT: ITOH, Naoto
APPLICANT: YONEHARA, Shin
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APPLICATION NUMBER:
MOLECULE TYPE:
                                                                                    SEQUENCE CHARACTERISTICS
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 NOACKPWINCIL 23
                  TOPOLOGY:
                                  STRANDEDNESS:
                                                                     LENGTH:
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                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: BIRCH, ST
STREET: P.O. BOX 747
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                                                     amino acid
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                                                                  133 amino acids
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protein
                                  single
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Pred. No.
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0.00013;
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RESULT 10
US-08-477-347-17
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Best Local Similarity
Watches 12; Conserva
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US-08-219-237B-8
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FILING DATE: 28-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,129
FILING DATE: 22-APR-1992
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: James W. Hellwege
REGISTRATION NUMBER: 28,808
REFERENCE/DOCKET NUMBER: 516762
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                          Sequence 17, Application US/08477347 Patent No. 6232446
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APPLICANT: ITOH, Naoto
APPLICANT: YONEHARA, Shin
TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
NUMBER OF SEQUENCES: 11
                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                             110 NOACKPWINCTL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUDRESSEE: James W. Hellwege
STREET: P.O. Box 2266 Eads Station
CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.0%; Ended to the conservative to the conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
   OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8, Application US/08219237B
o. 5874546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.3%; Score 12; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
                                    METT,
                                                              BELETSKY, Igor
                                                                                                   WALLACH, David
BIGDA, Jacek
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                             Igor
TNF LIGANDS
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Pred. No. 0.00039;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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J. 0.0004;
O;
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US-08-476-862-8
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 106

FILING DATE: 08-JUL-1993

ATTORNEY/AGENT INFORMATION:

NAME: TOWNSEND, G. KEVIN

REGISTRATION NUMBER: 34,03
                                                                                                                                                                                                                   APPLICANT: WALLACH, I APPLICANT: BIGDA, Ja APPLICANT: BELETSKY, APPLICANT: METT, Igo: APPLICANT: ENGELMANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: WALLACH-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
                                                                           STREET: 419 CONTROL WAShington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acid
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
OPERATING SYSTEM: PC-DOS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                              APPLICANT: ENGELMANN, Hartmut
TITLE OF INVENTION: TNF INHTE
                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           138 NOACKPWTNCTL 149
                                                                                                                                                                                                                                                                                                                                                                                                                            111 NOACKPWTNCTL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 140 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.
                                                                  ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/477,347
                                                                                                                                    419 Seventh Street, N.W.
                                                                                                                                                                                                                                        METT, Igor
                                                                                                                                                                                                                                                    BELETSKY, Igor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                      CH, David
, Jacek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
   PC-DOS/MS-DOS
                                                                                                                                                                                                       TNF INHIBITORS
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; 1
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RESULT 12
US-08-974-022-51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 51,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: IL 91229
FILING DATE: 06-AUG-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 90339
FILING DATE: 18-MAY-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                       APPLICANT: Boyle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
PRIOR APPLICATION UMBER: IL 107267
               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 06-APR-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 NOACKPWINCTL 122
                                                                                                                                                                                                                                                                ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
                                                                                                                                                                                                           COUNTRY: USA
ZIP: 91320-1789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25,
REFERENCE/DOCKET NUMBER:
                                     CLASSIFICATION:
                                                     APPLICATION NUMBER: US/0 FILING DATE: 12-DEC-1995
                                                                                                                                                                                                                                            STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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APPLICATION NUMBER: 08/577,788
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                                                                      US/08/974,022
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                                                          Matches
                                                                      Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Boyle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                         NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 'S
SEQUENCE CHARACTERISTICS:
                                                                                                                                             STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION: NAME: Winter, Robert B.
                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: Li
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135 NQACKPWTNCTL 146
                 138 NQACKPWINCIL 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1840 Dehavilland Drive CITY: Thousand Oaks STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 91320-1789
                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Winter, Robert B. REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                      Similarity
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                                                                                                                                                                                                          205 amino acids
                                                     ilarity 100.0%;
Conservative
                                                                                                                                                             SS: single
linear
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100.0%; Pred. No.
                                                                        4.3%; Score 12;
00.0%; Pred. No.
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RESULT 14 US-08-795-447A-51

Sequence 51,

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RESULT 15
US-08-974-186-51
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Best Local Similarity 100.0%; F
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                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                      Sequence 51,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprote
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                         APPLICANT: Boyle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/795,447A
ZIP: 91320-1789

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             135 NQACKPWTNCTL 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Amgen Inc.
STREET: One Amgen Center Drive
CITY: Thousand Oaks
STATE: California
                                                                                                                                    ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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                                                                                                    COUNTRY:
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                                                                                                                     California
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linear
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Release #1.0, Version #1.30
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; Pred. No.
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US-08-795-446B-51
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REFERENCE/DOCKET NUMBER: A-3
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 205 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 51, Appl Patent No. 628803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local Similarity 100.0%;
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                                                                            REFERENCE/DOCKET NUMBER: A INFORMATION FOR SEQ ID NO: 51: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Boyle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
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TOPOLOGY: 1
                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Winter, Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: OSTEOPROTEGERIN NUMBER OF SEQUENCES: 53
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TOPOLOGY: Li
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                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                          FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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                               STRANDEDNESS:
                                               TYPE:
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                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                              LENGTH:
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1840 Dehavilland Drive
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linear
                s: single
linear
                                                             amino acids
protein
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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0,

Query Match

4.3%;

Score 12;

DB 4;

Length 205

Pred. No.

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TOPOLOGY: linear

HOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-097-827-7
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US-08-494-574-7
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; Sequence 7, Application US/08097827

; GENERAL INFORMATION:
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                                                                                                                                                                        Sequence 7, Application US/08494574 Patent No. 5783665
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 206-587-0730
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 206 amino acids
TYPE: amino acid
            APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Fanslow, William
APPLICANT: Gayle, Richard
TITLE OF INVENTION: NO. 5783665el Cytokine Which is a Ligand for
TITLE OF INVENTION: OX40
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/097,827
FILING DATE: 23-Jul-1993
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                 138 NOACKPWINCTL 149
                                                                                                                                                                                                                                                                                             136 NOACKPWINCTL 147
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ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 2806 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goodwin, Ray
Fanslow, William
Gayle, Richard
TITLE OF INVENTION: Novel Cytokine Which is a Ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Baum, Peter
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ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                         4.3%; Score 12; DB 1; 1
100.0%; Pred. No. 0.00058
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hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11, Application GENERAL INFORMATION:
APPLICANT: Baum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local Similarity
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FILING DATE: 22-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA: 38-PPLICATION DATA: US/08/097,827
FILING DATE: 23-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: PERKINS, PATICIA A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 3806
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 206 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 NOACKPWINCTL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Imm
STREET: 51 Uni:
CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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                                                                          COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
FILLING DATE: 23-Jul-1993
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                               COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Novel Cytokine which is a Ligand for $\operatorname{\textsc{OX40}}$ NUMBER OF SEQUENCES: 13
                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98101
NAME: Perkins, Patricia A. REGISTRATION NUMBER: 34,693 REFERENCE/DOCKET NUMBER: 28
                                                                                                                                                                                                                                                                                             STATE: WA
                                                                                                                                                                                                                                                                                                                STREET: 51 Un:
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/08097827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 University Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baum, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goodwin, Ray
Fanslow, William
Gayle, Richard
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100.0%; Pred. No.
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; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 11: US-08-097-827-11
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                                                                                                                                       ; MOLECULE TYPE: protein US-08-494-574-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/08494574 Patent No. 5783665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity Matches 12; Conserv
                                                                                                                                                                                                                                            TELEPHONE: 206-587-0730 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Fanslow, William
APPLICANT: Gayle, Richard
TITLE OF INVENTION: No. 5783665el Cytokine Which is
TITLE OF INVENTION: OX40
                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
FILING DATE: 23-JUL-1993
ATTORNEY/AGENT INFORMATION:
ANALY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
138 NQACKPWINCTL 149
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                                                                                                                                                                                                                                                                                            NAME: Perkins, Patricia A. REGISTRATION NUMBER: 34,693 REFERENCE/DOCKET NUMBER: 28
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/494,574 FILING DATE: 22-JUN-1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                         LENGTH: 438 amino acids
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TELEPHONE: 206-587-0730
WATION FOR SEQ ID NO: 11:
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                                                                                                                                                                                      amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Immunex Corporation
51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                    Conservative
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                                                4.3%; Score 12;
100.0%; Pred. No.
ative 0; Mismatc
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100.0%; Pred. No.
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thes 0;
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0.0012;
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RESULT 22
US-08-995-659-15
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Best Local Similarity
"hehes 9; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-996-139-15
                                                                                                            Sequence 15, Application US/08995659 Patent No. 6242213
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                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (206)233-0644 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: USSN 08/813,509
FILING DATE: ,07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
               APPLICANT: Anderson, Dirk M. APPLICANT: Galibert, Laurent APPLICANT: Maraskovsky Eugene TITLE OF INVENTION: Ligand for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                        170 CKPWTNCTL 178
                                                                                                                                                                                                                                                             141 CKPWTNCTL 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,693 REFERENCE/DOCKET NUMBER: 2851-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operatin
SOFTWARE: Microsoft Word for Po
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/996,139 FILING DATE: 22 DECEMBER 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      625 amino acids
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/ 100.0%; Pr
Ligand for Receptor Activator of NF-kappaB : 19
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%; Pred. No. 1.3
0; Mismatches
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5. 1.3;
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RESULT 23
US-09-215-649A-15
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                                                                                                                                                                                                                                                                                                                                            Sequence 15, Application US/09215649A
Patent No. 6271349
GENERAL INFORMATION:
GBILDERT, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local :
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
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APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5\5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 CKPWTNCTL 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 3.2%; Score 9; DB 4; Local Similarity 100.0%; Pred. No. 1.3; es 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                              CITY: Seattle
STATE: WA
                                                                                                                                                                                                                        ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                      OF SEQUENCES:
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                                                                                                                                    USA
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; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-215-649A-15
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US-09-105-390-20
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                      FILING DAIL.

FILING DAIL.

CLASSIFICATION:

PRIOR APPLICATION UNDER: 60/050,675

APPLICATION NUMBER: 60/050,675

FILING DATE: 25-JUN-97

FATTORNEY/AGENT INFORMATION:

NAME: Petithory, Joanne R.

NAME: Petithory, Joanne R.

NAME: Petithory, Joanne R.

NAME: 2000-0455.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 15:
      REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rodriguez, Raymond TITLE OF INVENTION: Rice Beta-TITLE OF INVENTION: and Genes NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170 CKPWTNCTL 178
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                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/1 FILING DATE: Filed herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 350 Caml
CITY: Palo Alto
STATE: CA
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FILING DATE: CUNKNOWN>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
FILING PATRICON NUMBER: 34,693
FILING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: Apple Operating System 7.5.
SOFTWARE: Microsoft Word for Power Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,649A
FILING DATE: 17-Dec-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 625 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
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Indels

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GENERAL INFORMATION:
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 3148
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 17
LENGTH: 105
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                  RESULT 26
US-09-124-671-19
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Best Local Similarity
"~+~hes 7; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-124-671-17
: Sequence 17, Application US/09124671A
: Patent No. 6160088
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                                                                                                                GENERAL INFORMATION:
APPLICANT: ROTHMAN, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
                                                                                                                                                                                                      Sequence 19, Application US/09124671A Patent No. 6160088
                                      CURRENT APPLICATION NUMBER: US/09/124,671A CURRENT FILING DATE: 1998-07-29 NUMBER OF SEQ ID NOS: 42 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 7; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
ORGANISM: Artificial Sequence
               LENGTH: 109
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 AALLLLG 19
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TELEX:
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linear
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0; Mismatches
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Pred. No.
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RESULT 27
US-09-124-671-21
; Sequence 21, Applica
; Patent No. 6160088
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                                                                           ; OTHER INFORMATION: chimeric rat comp US-09-124-671-13
                                                                                                                                                                                                                                                                                                                                                                       RESULT 28
US-09-124-671-13
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Best Local Similarity
'thas 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Rothman, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 21
LENGTH: 109
TYPE: PRT
                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 13
LENCTH: 115
TYPE: PRT
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Best Local S
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              Query Match
Best Local
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APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/124,671A CURRENT FILING DATE: 1998-07-29 NUMBER OF SEQ ID NOS: 42
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                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                            FEATURE:
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 Similarity 100 7; Conservative
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2.5%; Score 7; DB 4
100.0%; Pred. No. 24;
tive 0; Mismatches
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100.0%; Pred. No.
Live 0; Mismatc
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Pred. No.
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US-08-478-039-110
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US-09-124-671-15
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Best Local S
Matches 7
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CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 15
LENGTH: 115
TYPE: PRT
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             CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072

FILLING DATE: 25-JAN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292

FILLING DATE: 10-JUL-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281

FILLING DATE: 23-MAR-1992

PRIOR APPLICATION DATA:
APPLICATION DATA:
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APPLICATION DATA:
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APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,039
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 22313-1404
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CITY: Alexandria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.5%; Score 7; DB . 100.0%; Pred. No. 24 tive 0; Mismatches
US 07/735,064
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Search completed: June 18, 2002, 14:28:49 Job time: 207 sec
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                 TELEPHONE: 703-836-6620
TELEPAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
                                                                              15 ALLLLGL 21
|||||||
4 ALLLLGL 10
                                                                                                                                                                                                                                                                     TYPE: amino acid TOPOLOGY: linear
                                                                                                                                        2.5%;
Similarity 100.0%;
7; Conservative (
                                                                                                                                                     0
                                                                                                                                                 Score 7; DB 1;
Pred. No. 26;
0; Mismatches
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Gaps

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Result
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq length: 0 seq length: 2000000000
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SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:

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SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1988.DAT:

SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:

SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:

SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:

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Copyright (c) 1993 - 2000 Compugen Ltd.
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ACT-4 h-1 receptor
Human Ox40 protein
Human tumour necro
Deduced sequence
TNF-R extracellula
Human TNF-R extrac
Secondary signalli
Human secondary si
Amino acid sequenc
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2851	ABG01306	254	63	AAB53079	AAB80233	AAU12327	AAM38847	AAY95342	AAB24398	AAY97290	AAY13365	AAY32926	ABG28519	AAM95526	ABG18405	AAW75070	ABG01305	AAW87708	ABG01184	6	ABG01304		AAE01994	AAE04427	AAE08739	64		829		Ψ	50	S	88	897	æ	AAB66985	7	82
1 human	Novel human diagno	an	уpе		PRO224	PRO224	polypeptide	PRO224	PRO224 prot	associa	Amino acid sequenc	Transmembrane doma	Novel human diagno	Human reproductive	human	=	human		1 human	1 human	Novel human diagno	acroso	င္က	receptor a	receptor a	e receptor	nding p	NF-kB	NF-kB rec	ine ostec	ding prote		3	e OX40 ext	se	Ox40 protein. Uni		Human secondary si

## ALIGNMENTS

AAR74737

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AAR74737 standard; Protein;

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AAR74737;

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W09512673-A
                                                                       Cleavage-site
                                                                                      Cleavage-site
                                                                                                                                              Cell surface receptor; ACT-4; T-lymphocyte; T-cell; immune system
                        Domain
                                       Modified-site
                                                      Modified-site
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                                                                                                               Key
                                                                                                                               Homo
                                                                                                                                                             ACT-4 cell surface receptor protein
                                                                                                                                                                               21-NOV-1995 (first entry)
                                                                                                                              sapiens.
                       /note= "glycosylation site" 214..240
                                      /note= "glycosylation site" 160..162
                                                                                      /note= "signal peptide"
22..23
                                                                      /note= "signal cleavage site"
24..25
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                                                                                                               Location/Qualifiers
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                                                              "signal cleavage site"
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                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated ACT-4 receptor antibodies, useful for t
                                           grait versus host disease; immune response; transplantation; autoimmune disease; inflammation; HIV; human immunodeficiency virus; HTLV; human T lymphocyte virus; inflammatory bound disease.
                                                                          ACT-4; specific binding partner; sbd; B cells; lymphocyte;
                                                                                                                                                     AAR79904 standard;
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Location/Qualifiers
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(STRD )
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                                                                                 pgvdcapcppghfspgdnqackpwtnctlagkhtlqpasnssdaicedrdppatqpqetq\\
                                                                                            PGVDCAPCPPGHFSPGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPATQPQETQ
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UNIV LELAND STANFORD
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No. 2.7e-250;
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18-AUG-1999;
20-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences of the human tumour necrosis factor receptors TR13 and TR14. These sequences are useful in the diagnosis and treatment of many diseases, including cancer autoimmune diseases, cardiovascular disorders, allergies, neurodegenerative diseases, graft rejection, inflammation, aneurysms and infortune to the contraction of the contract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding 2 human tumor necrosis factor receptor polypeptides ((TRI3)) and (TRI4)), useful for the prevention, diagnos and treatment of, e.g. cancers, acquired immune deficiency syndrome hypohidrotic ectodermal dysplasia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumour necrosis factor receptor; TR13; TR14; autoimmune disease; allergy; inflammatory d. rejection; apoptosis; cardiovascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                           The present invention describes the human TRID protein (tumour necrosis of factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without intracellular domain, also referred to as tumour necrosis factor of TRAIL) receptor s (TNRF-5 or TRS)). TRID has cytostatic, immunosuppressive, conotropic, neuroprotective, antiviral, antiinflammatory, anticonvulsant, cardiant, anti-HIV, antiparkinsonian and vasotropic activities, and can be used in gene therapy. The TRID polynucleotides care useful for detecting complementary polynucleotides. TRID proteins and complementary polynucleotides are useful for inducing proliferation of T-cells, endothelial colls and certain haematopoietic cells, to regulate antiviral responses cand to prevent certain autoimmune diseases after stimulation of TRID by cardiated with increased or decreased apoptotic cell death. The TRID collynucleotides, proteins, antibodies, agonists and antagonists are useful in the diagnosis, treatment or prevention of: (a) cancer; (c) diseases associated with increased compensis, utenament or prevention of: (a) cancer; (b) autoimmune disorders; (c) diseases associated with increased in comparison with TRID in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunosuppressive; neuroprotective; antiviral; antiinflammatory; anticonvulsant; antiparasitte; cardiant; anti-HTV; antiparkinsonian; gene therapy; restenosis; graft versus host disease; tumour; cancer; apoptotic cell death related disease; autoimmune disorder; cardiovascular disorder; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid encoding a TRID polypeptide, also referred to as necrosis factor receptor 5, useful in the diagnosis, treatment prevention of cancer, autoimmune disorders and viral infection
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   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 2; 285pp; English.
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RESULT
AAR76996
the Ox-40 antigen was identified (expressed on the surface of activated autoantigen-specific CD4+ T-cells present at the site of inflammation but absent on CD4+ T-cells at non-inflammatory sites) and cDNA encoding the antigen was isolated. PCR primers were designed and used to clone murine Ox-40 cDNA by PCR from RNA isolated from murine CD4+ T-cells activated with concanavalin A. Then the murine Ox-40 cDNA was used to probe a cDNA lambda gtll library from human activated T lymphocytes to obtain human Ox-40 cDNA. The published patent application states that the Ox-40 cDNA sequence is also in SQ ID no. 1, but this sequence is not present in the spec. A nucleic acid having the sequence in SQ ID no 1 and
                                                                                                                                                                                                                                                                      Antigen OX-40 is specifically expressed on the cell surface of antigen activated T-cells. A pluman cDNA encoding the human OX-40 homologue was cloned as follows. Using the Experimental Autoimmune Encephalomyelitis model in rats
                                                                                                                                                                                                                                                                                                                                                                                                Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid encoding an activated T-cell antigen, Ox-40 - used develop prods. for detection and therapy of conditions mediated activated T-cells, eg. multiple sclerosis, rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-FEB-1995;
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                                                                                                                                                                                                                                                                                                                                                                                             English.
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Best Local S
Matches 114
                                                                        The present invention describes peptides and peptide analogues which correspond in primary sequence to a binding loop of a tumour necrosis factor receptor (TNF-R) superfamily member. The compounds are especially designed from a binding loop of TNF-R p55. They are capable of inhibiting TNF binding to its cellular receptors and may be used to inhibit the biological activities of TNF-They may be used in treating TNF-associated conditions such as scute and chronic inflammatory responses, septic shock, cachexia, autoimmunity, graft-versus-host disease, skin allergic reactions, immune complex disease, transplantation rejection and malaria. Administration is, e.g. oral,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumour necrosis factor receptor; TNF-R; autoimmune diseases; inflammation; septic shock; cachexia; graft versus host disease; skin allergic reaction; immune complex disease; malaria;
                        sequence represents present invention.
                                      transdermal, transmucosal, pulmonary, subcutaneous, intravenous intramuscular. Parenteral dosage is 0.1-5 mg/kg/day. The present sequence represents an extracellular Cys-rich domain of TNF-R fr
                                                                                                                                                                                                                                                              New compounds designed from a binding loop of a tumour necrosis factor receptor - are capable of inhibiting the biological activities of tumour necrosis factor, e.g., in treating inflamm
                                                                                                                                                                                                                                                                                                                                             Greene
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                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                      or autoimmune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNF-R extracellular
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                                                                                                                                                                                                                                                                                                                                                                       (UYPE-) UNIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transplantation rejection.
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                                                                                                                                                                                                                                                                                                                     1999-080781/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                         Fig 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                                                                                                                                                                                                                        PENNSYLVANIA.
                                                                                                                                                                                                                                                                                                                                                                                                 97US-0866545
                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-US10891
                                                                                                                                                                                                                         78pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cys-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domain 0x40
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Pred. No.
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s 0;
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                                                                                                                                                                                                                                                                   inflammation
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                                       from the
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                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYPE-)
                                                                                                                                                and immunomodulatory activities, and are tumour necrosis factor (TNF)-
related activation-induced cytokine (TRANCE)/ receptor activator of
NF-kappaB ligand (RANK) inhibitors. The method is useful for treating
diseases characterised by bone loss such as osteoporosis, Paget's
disease, metastatic bone disease, rheumatoid arthritis or periodontal
                                                                                                                                                                                                                   osteoclastogenesis and bone resorption. Osteoclastogenesis and bone resorption inhibiting peptide analogues from the present invention have osteopathic, cytostatic, antirheumatic, antiarthritic, antiinflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             osteoclastogenesis; bone loss; bone resorption; osteopathic; cytost antirheumatic; antiarthritic; antilarflammatory; immunomodulatory; tumour necrosis factor-related activation-induced cytokine; TRANCE; receptor activator of NF-kappaB ligand; RANK; osteoporosis;
                                                       Sequence
                                                                                           disease, and modulating dendritic cell maturation, T cell proliferation, and/or CD40 receptor systems. The present sequence represents an extracellular Cys-rich domain of a tumour necrosis factor receptor (TNF-R) superfamily member, which is used in the exemplification of
                                                                                                                                                                                                                                                                The
                                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                       Aoki K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     periodontal disease; modulating dendritic cell maturation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Paget's disease; metastatic bone disease; rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumour necrosis factor receptor; TNF-R; inhibition; osteoclast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human TNF-R extracellular Cys-rich domain OX40 SEQ ID NO:10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB69201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB69201 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                  (BARO/)
                                                                                                                                                                                                                                                                                                                                                                                                                               (HORN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64
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                                                                                                                                                                                                                                                               present invention describes a method for inhibiting
                                                                                                                                                                                                                                                                                                                 of peptides and peptide analogs which are {\tt TRANCE/RANK} inhibitors, inhibiting osteoclastogenesis and bone resorption -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDSY 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                         JNIV
AOKI K.
PORNE W C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proliferation; CD40 receptor system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNIV PENNSYLVANIA
                                                                                                                                                                                                                                                                                                                                                                                       Horne WC,
                                                       58
                                                                                                                                                                                                                                                                                         Fig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0146090
                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                       81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                       Baron
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 15.2%;
                                                                                                                                                                                                                                                                                                                                                                                     70,
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Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                       Greene MI,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
               DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.4e-44;
                                                                                                                                                                                                                                                                                                                                                                                     Murali
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       osteopathic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
              Length 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arthritis;
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1.7e-31;

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241 RRDQRLPPDAHKPPGGGSFRTPIQEEQADAHSTLAKI

Query Match Best Local S Matches 37

137; Conservative

13.4%; 5c. 100.0%; Pr

Score 37; DB Pred. No. 5.3

DB 22; 5.3e-27

Length 37;

Indels

0;

Gaps

0

.3e-27;

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AAB84272
ID AAB8
 RESULT
                                                                     The present sequence represents a secondary signalling sequence, which is linked to a non-natural stimulatory primary signalling motif to produce a cytoplasmic signalling motif. The primary motif is efficient at mediating immune cell signal transduction, particularly when incorporated in an intracellular signalling domain of a chimeric receptor. The primary signalling motif can be combined in any way so as to achieve the desired level of activation (or inhibition) of a number of secondary messenger cascades. The signalling motifs are useful in therapy and in the manufacture of medicament for treating or preventing disease in humans or animals. They are are useful for treating human patients suffering from infections diseases e.g. human immunodeficiency virus (HIV) infections, inflammatory/autoimmune diseases such as asthma and eczema, congenital diseases e.g. cystic fibrosis, sickle cell anemia, dermatological diseases e.g. psoriasis, neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                              Novel o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dermatological disease; psoriasis; neurological diseas multiple sclerosis; transplant-related disease; metabo organ transplant rejection; graft versus host disease;
                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chimeric receptor; inflammatory disease; autoimmune disease; ast eczema; congenital disease; cystic fibrosis; sickle cell anemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stimulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Secondary signalling sequence used to make cytoplasmic signalling motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB84272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB84272
Sequence
                                                            sickle cell anemia, dermatological diseases e.g. psoriasis, neurological diseases e.g. multiple sclerosis, transplant-related disease e.g. organ
                                                                                                                                                                                                                                                                                                                                                                                                                                         Finney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200132709-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             idiopathic disease; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-AUG-2001
                                             transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CELL-) CELLTECH CHIROSCIENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64
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                                                                                                                                                                                                                                                                                                                                           cytoplasmic signalling protein and chimeric receptor prolifer treating HIV infection, asthma, eczema, psoriasis, osis, contain non-natural stimulatory primary signalling
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MH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
 37
                                           rejection, graft versus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     primary signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                 29;
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                                                                                                                                                                                                                                                                                                             45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide;
                                cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer.
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                                               host
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                                             disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            metabolic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease;
                                               metabolic/idiopathic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        signal transduction;
                                                                                                                                                                                                                                                                                                                                                                         protein,
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AAB98799
                                                                                                           The invention relates to a novel nucleic acid encoding an adaptor CC receptor protein comprising an extracellular ligand-binding domain, a CC transmembrane domain and an intracellular signalling domain. The CC intracellular signalling domain comprises the cytoplasmic portion of at CC least one adaptor protein, and the extracellular ligand-binding domain CC is not CDB or a major histocompatibility complex (MHC) class I protein. CC The adaptor receptor protein and the nucleic acid encoding it are useful in therapy. They are useful in the manufacture of a medicament for the CC treatment or prevention of disease in humans and animals. They are useful in the treatment of infectious diseases (e.g. HIV infection).

CC congenital diseases (e.g. cystic fibrosis and sickle cell anaemia).

CC dermatological diseases (e.g. psoriasis), neurological diseases (e.g.) cultiple sclerosis), organ transplant rejection, graft-versus host components of the adaptor receptor protein of the invention. Secondary signalling motif used in the CC invention. Secondary signalling motif used in the components of the adaptor receptor protein of the invention. Motifs were isolated from CD28, CD134 and CD154.
               Query Match
Best Local
 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antisickling; antipsoriatic; neuroprotective; immunosuppressive; antidiabetic; cytostatic; HY infection; inflammation; autoimmune disease; cystic fibrosis; sickle cell anaemia; psoriasis; neurological disease; organ transplant rejection; diabetes; cancer; graft-versus-host disease; adaptor receptor protein; CD28; CD134; CD
                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 26; Page 35; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fibrosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-328790/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primary signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human secondary signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB98799 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CELL-) CELLTECH CHIROSCIENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polynucleotide encoding adaptor receptor protein useful for
ing human immunodeficiency virus (HIV) infection, asthma, cystic
usis, multiple sclerosis, organ transplant rejection, diabetes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 Similarity
37; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anti-HIV; antiinflammatory; antiasthmatic; dermatological;
                                                                                   37
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lawson ADG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      motif; secondary signalling motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide;
                 13.4%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         motif SB34a.
 0
Score 37; DB; Pred. No. 5.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37
               DB 22;
5.3e-27;
                               Length 37;
 Indels
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Gaps
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Matches

Similarity 37; Conser

13.4%; nilarity 100.0%; Conservative

.08:

Score 37; DB Pred. No. 5.8 0; Mismatches

.8e-27;

Length 41; Indels

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Gaps

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241 RRDQRLPPDAHKPPGGGSFRTPIQEEQADAHSTLAKI 277

rrdqrlppdahkppgggsfrtp1qeeqadahstlaki 39

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AAB84292
ID AAB8
XX AAB8
XX AAB8
XX AAB8
XX Stim
XXW Stim
XXW Coim
XXW Coim
XXW Coim
XXW Idic
XX Synt
XX WO20
PN WO20

                                                      CC The present sequence represents a secondary signalling sequence, which may be linked to a non-natural stimulatory primary signalling motif CC The primary motif is efficient at mediating immune cell signal CC transduction, particularly when incorporated in an intracellular CC can be combined in any way so as to achieve the desired level of CC can be combined in any way so as to achieve the desired level of CC can be combined in any way so as to achieve the desired level of CC retivation (or inhibition) of a number of secondary messenger cascades. The signalling motifs are useful in therapy and in the manufacture of CC medicament for treating numan patients suffering from infectious are are useful for treating human patients suffering from infectious diseases e.g. human immunodeficiency virus (HTV) infections, congenital CC diseases e.g. psorlasis, neurological diseases e.g. multiple sclerosis, transplant-related disease e.g. organ transplant rejection, graft versus CC constitutions metabolic/idiopathic disease e.g. diabetes, and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel cytoplasmic signalling protein and chimeric receptor protein, useful for treating HIV infection, asthma, eczema, psoriasis, multiple sclerosis, contain non-natural stimulatory primary signalling motif -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stimulatory primary signalling motif; immune cell; signal transduc chimeric receptor; inflammatory disease; autoimmune disease; asthm eczema; congenital disease; receptor; sickle cell anemia; dermatological disease; psoriasis; neurological disease; multiple sclerosis; transplant-related disease; metabolic disease; organ transplant rejection; graft versus host disease; organ transplant rejection; graft versus host disease;
       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Fig 4; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-389718/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of a secondary signalling sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB84292 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CELL-) CELLTECH CHIROSCIENCE LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               idiopathic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41
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                                                                                                                                             when incorporated into an intracellular signalling domain of a chimeric receptor. Nucleic acids that encode, and polypeptides that contain, these primary signalling motifs are useful in medicine and research. They are useful in therapy, or in the manufacture of a medicament for treating or preventing disease in humans or in animals. These diseases include infections (e.g. HIV (human immunodeficiency virus) infection), inflammatory or autoimmune diseases (e.g. asthma or eczema), congenital diseases (e.g. cystic fibrosis or sickle cell anaemia), dermatological diseases (e.g. psoriasis), neurological diseases (e.g. multiple sclerosis), organ transplant rejection or graft versus-host disease, or metabolic/idiopathic diseases (e.g. diabetes or cancer). The present sequence is one of a large number of primary and secondary signalling motifs used in the invention. Primary signalling motifs are sequences that transduce either a stimulatory or an inhibitory signal, which regulates primary activation of the T cell receptor (TCR) complex. Secondary motifs impart secondary or co-stimulatory signalling capacity to a molecule in T cells. GS linkers have been incorporated at each
                                  Query Match
Best Local
Matches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to novel primary signalling motifs containing a consensus amino acid sequence. These motifs are extremely efficient at mediating immune cell signal transduction, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acids encoding polypeptides with expanded primary signaling motifs, for use in gene therapy, particularly for treating or preventing infections, inflammations or autoimmune diseases in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; primary signalling motif; sequence block; SB; immunosuppressive; secondary signalling sequence; antimicrobial; antiinflammatory; dermatological; neuroprotective; cytostatic; anti-HIV; antiasthmatic; antisickling; antipsoriatic; antidiabetic; gene therapy; diabetes;
                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Finney HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immune cell signal transduction; infect autoimmune disease; congenital disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB98777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB98777 standard; Peptide; 41 AA
 241 RRDQRLPPDAHKPPGGGSFRTPIQEEQADAHSTLAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-328791/34
                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lawson ADG
                                                                                                                        41
                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43pp; English.
                                                  13.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            motif sequence block
                                  0
                                                Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LTD
                                   Mismatches
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                                                    5._
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       psoriasis;
                                                  .8e-
                                                                Length 41
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RESULT J
AAB988222
AD HUMM
KW AUTHOR AUTHOR
KW AUTHOR
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                                                                                          multiple sclerosis), organ transplant rejection, graft-versus-host disease and metabolic/idiopathic diseases such as diabetes and cancer. The present sequence is one of a number of sequence blocks (SBs) of primary and secondary signalling motifs. Primary signalling motifs transduce either a stimulatory or an inhibitory signal, which regulates primary activation of the T cell receptor (TCR) complex. Secondary signalling motifs impart secondary cro-stimulatory signalling capacity to a molecule in T cells. Primary and secondary signalling motifs may be used as components of the adaptor receptor protein of the invention. The sequence contains a GS linker at the N-terminus to
                                                                                                                                                                                                                                                                                                                                                                                                                                        The adaptor receptor protein and the nucleic acid encoding it are useful in therapy. They are useful in the manufacture of a medicament for the treatment or prevention of disease in humans and animals. They are useful in the treatment of infectious diseases (e.g. HIV infection), inflammatory and autoimmune diseases (e.g. asthma and eczema), congenital diseases (e.g. cystic fibrosis and sickle cell anaemia), dermatological diseases (e.g. psoriasis), neurological diseases (e.g.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel nucleic acid encoding an adaptor receptor protein comprising an extracellular ligand-binding domain, a transmembrane domain and an intracellular signalling domain. The intracellular signalling domain comprises the cytoplasmic portion of at least one adaptor protein, and the extracellular ligand-binding domain is not CD8 or a major histocompatibility complex (MIC) class I protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antisickling; antipsoriatic; neuroprotective; immunosuppro
antidiabetic; cytostatic; HIV infection; inflammation;
autoimmune disease; cystic fibrosis; sickle cell anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polynucleotide encoding adaptor receptor protein useful for treating human immunodeficiency virus (HIV) infection, asthma, cy; fibrosis, multiple sclerosis, organ transplant rejection, diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neurological disease; organ transplant rejection; diabetes;
graft-versus-host disease; adaptor receptor protein; sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB98822 standard; Peptide; 41
   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; anti-HIV; antiinflammatory; antiasthmatic; dermatological;
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   41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SB34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           psoriasis;
                                                                                                                                                                          fs may be
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                                                            when incorporated into an intracellular signalling domain of a chimeric creceptor. Nucleic acids that encode, and polypeptides that contain, these primary signalling motifs are useful in medicine and research. They are useful in therapy, or in the manufacture of a medicament for treating or preventing disease in humans or in animals. These diseases include infections (e.g. HIV (human immunodeficiency virus) infection), inflammatory or autoimmune diseases (e.g. asthma or eczema), congenital diseases (e.g. cystic fibrosis or sickle cell anaemia), dermatological diseases (e.g. psoriasis), neurological diseases (e.g. multiple sclerosis), organ transplant rejection or graft-versus-host disease, or metabolic/idiopathic diseases (e.g. diabetes or cancer). The present sequence is a secondary signalling sequence used in the co-stimulatory signalling capacity to a molecule in T cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; primary signalling motif; CD28; CD134; CD154; sequence block; SB; immunosuppressive; secondary signalling sequence; antimicrobial; cancer; antiinflammatory; dermatological; neuroprotectne; cytostatic; anti-HTV; antiasthmatic; antisickling; antipsoriatic; antidiabetic; gene therapy; diabetes; immune cell signal transduction; infection; inflammation; autoimmune disease; congenital disease; psoriasis; neurological disease;
                                                                                                                                                                                                                                                                                         efficient at mediating immune cell signal transduction, particularly when incorporated into an intracellular signalling domain of a chime
                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                   preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acids encoding polypeptides with expanded primary signaling motifs, for use in gene therapy, particularly for treating or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB98752 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CELL-) CELLTECH CHIROSCIENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200132867-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secondary signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB98752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241
                                                                                                                                                                                                                                                                                                                               consensus amino acid
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                                                                                                                                                                                                                                                                                                                                                                                   16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                 Page
                                                  signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                   infections,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lawson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                             relates to novel primary signalling motifs co mino acid sequence. These motifs are extremely
                                                                                                                                                                                                                                                                                                                                                                                 28;
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                                                                                                                                                                                                                                                                                                                                                                                 43pp; English
                                                  sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammations or autoimmune diseases in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   motif SB34a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 AA.
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                                                  isolated from human CD28, CD134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.8e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39
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                                                                                                                                                                                                                                                                                                                                             motifs containing
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Query Match,

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Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                        The present invention relates to a method for treating conditions leading to bone loss. The method comprises administering a purified and isolated osteoprotegerin (OPG) protein (AAF57836-AAF57838 and AAB66974-AAB66976) in conjunction with other substances such as tumour necrosis factor-alpha (TNF-alpha) inhibitors, interleukin (IL)-6. 8 and -18 inhibitors, ICE modulators, fibroblast growth factor (FGF)1-10 modulators and/or platelet activating factor (PAF) antagonists. The method is useful for treating conditions leading to bone loss such as rheumatoid arthritis, multiple sclerosis, osteoprosis, osteomyelitis and asthma. The method is also useful for treating inflammation, systemic lupus erythematosus (SLE) and graft-versus-host disease (GVHD). Other diseases that can be treated include acute pancreatitis, Alzhelmer's disease, anorexia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0x40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treating conditions leading to bone loss sucmultiple sclerosis and asthma, comprises and osteoprotegerin protein in conjunction with interleukin and tumor necrosis factor alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia; multiple sclerosis; osteoprocesis; osteomyelitis; asthma; inflammation; systemic lupus erythematosus; graft-versus-host disease; septic shock; acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; paccoronary condition; myocardial infarction; cancer; diabetes; psoriasis endometriosis; fever; glomerulonephritis; inflammatory bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-103031/11.
Sequence
                                                                                                                                                                                   include acute pancreatitis, Alzheimer's disease, anorexia, atherosclerosis, coronary conditions (e.g. myocardial infarction), cancer, diabetes, endometriosis, fever, glomerulonephritis, hypera inflammatory bowel disease, ischaemia, pain, Parkinson's disease, disease, pain, Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boyle WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JUL-1999;
09-DEC-1999;
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                                                                                                                                        inflammatory bowel disease, psoriasis and septic shock.
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    205
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99US-0457647
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disease;
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                                                OX40; cytokine; OX40/Fc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glycoprotein cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence encodes the extracellular domain of OX40, a membrane glycoprotein present on the CD4 positive subset of activated T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated DNA encoding the OX40 ligand polypeptide - also ve and host cells, used to produce recombinant ligand used in e.g. prim. T cell culture, to modulate immune response etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US5457035-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR81881 standard; Protein;
  Mus sp
                                                                                                                                                                                                              AAW48977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OX40; OX40-L; cytokine; cell surface molecule; membrane glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse type-II membrane polypeptide OX40 extracellular domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR81881;
                                                                                                                    Mouse 0X40 extracellular domain
                                                                                                                                                                  25-SEP-1998
                                                                                                                                                                                                                                                          AAW48977 standard; Protein; 206 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138
                                                                                                                                                                                                                                                                                                                                                                              136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100 nes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PR,
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DB; AATOO826.
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                                                                                                                                                                                                                                                                                                                                                                            ngackpwtnctl 147
                                                                                                                                                                                                                                                                                                                                                                                                                          NOACKPWINCTL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Column 33-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fanslow WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                        н
                                                                 cell antigen; TH-2 immune response; OX40-L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.3%; Sur
100.0%; Pr
.... 0;
                                                                                                                                                                entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gayle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 12;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ΑA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 16;
0.0048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          $\times CCCCCCCCCX\times \times \tin \times \times \times \times \times \times \times \times \times 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents the mouse OX40 extracellular domain The extracellular domain of OX40 is its ligand binding domain. The cDNA (AAV32640) encoding OX40 extracellular domain was used in the construction of the chimeric OX40/Fc cDNA (AAV32640). The invention claims for a murine OX40-L cytokine (AAW48975) that binds to the OX40 murine T cell antigen. The OX40-L protein is claimed to be useful for co-stimulation of T-cell production and in binding assays for detecting OX40 for its homologues. The OX40-L protein is also claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUL-1993;
22-JUN-1995;
WPI; 1995-357992/46.
N-PSDB; AAT00829.
                                                                                                                                                                                                                                                                                                                                                                                             OX40; OX40-L; cytokine; cell surface molecule; pDC406/OX40/Fc*; membrane glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencé
                                                                    Baum PR,
                                                                                                                                                             23-JUL-1993;
                                                                                                                                                                                                         23-JUL-1993;
                                                                                                                                                                                                                                                       10-OCT-1995.
                                                                                                                                                                                                                                                                                                   US5457035-A.
                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid pDC406/0X40/Fc*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR81882 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Col 33-34; 26pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JUN-1995;
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                                                                                                               ( VMMI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to generate a TH-2 immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 NQACKPWINCTL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 ngackpwtnctl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1998-427099/36.
DB; AAV32640.
                                                                                                                  IMMUNEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide OX-40 ligands - for on and binding assays for OX-40 a
                                                                    Fanslow WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fanslow WC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                             93US-0097827
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95US-0494574
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                                                                                                                  CORP
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                                                                    Gayle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding an OX40/Fc mutein protein.
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                                                                    RВ,
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Pred. No.
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                                                                    Goodwin
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. 0.0048;
ches 0;
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                                                                    RG
                                                                                                                                                                                                                                                                                                                                                                                                                     plasmid;
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RESULT 1
AAW48976
A PRESENTATION OF THE PROPERTY OF THE PROPERTY
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Best Local S
Matches 12
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Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This plasmid encodes an OX40/Fc antibody fragment mutein protein, and is used to express a soluble OX40/Fc mutein fusion protein for use in detecting cDNA clones encoding a OX40 ligand. The Fc fragment may be derived from human IgG1, and the plasmid may be used to transform the CV-1/EBNA (ATCC CRL 10478) monkey kidney cell line. Culture supernatant was purified by affinity chromatography and this was used, together with labeled goat anti-human IgG to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
Region
WPI; 1998-427099/36
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and
                                       Baum
                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OX40/Fc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OX40/Fc mutein
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                                                                          (IMMV ) IMMUNEX CORP
                                                                                                                     23-JUL-1993;
22-JUN-1995;
                                                                                                                                                                              22-JUN-1995;
                                                                                                                                                                                                                     21-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136
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                                       PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ngackpwtnctl 147
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                                                                                                                   93US-0097827
95US-0494574
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225
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                                                                                                                                                                                                                                                                                                                                                                              /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1..206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                   "changed
mutant"
                                                                                                                                                                                                                                                                                                  "changed
mutant"
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mutant"
                                       Gayle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Mutant Fc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigen; TH-2 immune response; OX40-L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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Pred. No.
                                       RВ,
                                                                                                                                                                                                                                                                                                                                                                              from
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                                       Goodwin
                                                                                                                                                                                                                                                                                                                      Gly
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0.0091;
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                                       RG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IgG1
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RESULT 1
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Best Local S
Matches 12
                     preventive and/or treating as osteoporosis. Substance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents the OX40/Fc fusion protein that contains the extracellular domain of mouse OX40 fused to the mutated Fc region of the human IgGl antibody. The fusion protein was used for detecting cDNA clones encoding an OX40 ligand. The invention claims for a murine OX40-L cytokine (AAW48975) that binds to the murine T cell antigen, OX40. The OX40-L protein is claimed to be useful for co-stimulation of T-cell production and in binding assays for detecting OX40 or its homologues. The OX40-L protein is also claimed to generate a TH-2 immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAV32636
                                                                                                                                                                                                                                                                                                                                                OBM-BP; OBM binding bone metabolic disea
                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Purified polypeptide OX-40 ligands - for co:stimulation of T-cell production and binding assays for OX-40 and homologues
Sequence
                                                                                                Claim 1; Page 17-18; 18pp; Japanese.
                                                                                                                           A new
                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                           07-DEC-1999
                                                                                                                                                                                                                                                                                                 JP11332581-A
                                                                                                                                                                                                                                                                                                                         Mus sp
                                                                                                                                                                                                                                                                                                                                                                                    OBM binding protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY59508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY59508 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Col 37-40;
                                                                                                                                                                                   (SNOW ) SNOW BRAND MILK PROD CO (SANY ) SANKYO CO LTD.
                                                                                                                                                                                                                          24-MAR-1998;
                                                                                                                                                                                                                                                  20-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19
                                                                                                                                                  2000-091362/08
DB; AAZ49022.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ngackpwtnctl 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOACKPWINCIL 149
                                                                                                                          protein, a DNA and its application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   438 AA;
  201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                               nding protein; osteoclast formation disease; osteoporosis; therapy.
                                                                                                                                                                                                                          98JP-0076232
                                                                                                                                                                                                                                                  98JP-0316973
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein; 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.3%;
                                   osteoclast formation promoting factor (OBM)

BP) of the invention. The protein is useful as a sating agent for bone metabolic diseases such as sees which inhibit the binding of OBM to OBM-BP ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26pp; English.
                        reagents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 12; DB Pred. No. 0.(
                                                                                                                                                                                                   LTD.
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0.0091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 438;
                                                                                                                                                                                                                                                                                                                                                            promoting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                      to OBM-BP can
                                                                                                                                                                                                                                                                                                                                                             factor;
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Query Match Best Local Similarity

3.2%;

Score Pred.

9; DB No. 3;

21;

Length 201;

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RESULT :
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                                               The present sequence represents murine osteoclast differentiation can dactivation receptor (ODAR). The present invention describes costeoprotegerin (OPG) binding protein. Host cells transfected with vectors containing nucleic acid molecules encoding OPG binding protein care used to produce recombinant OPG binding protein. OPG binding protein cis used in binding assays to determine osteoprotegrin (OG) in biological cand antagonists, including intracellular protein); to raise Ab (useful cin immunoassays for detection of OPG binding protein) and to identify compounds that modulate binding of OPG binding protein to ODAR. The culcic acid molecule encoding OPG binding protein to DDAR. The culcic acid molecule encoding OPG binding protein can be used to detect COPG binding protein encoding sequences, e.g. screening for related complementary sequences, also to produce transgenic animal models, while complementary sequences are used for antisense regulation of OPG binding protein complementary soluble forms of OPG binding protein or Ab, are used to treat or prevent bone contenses, hypercalcaemia, Paget's disease, periodontal disease, with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-1998;
16-APR-1997;
23-JUN-1997;
                osteoporosis, lousure that promote
                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid encoding osteoprotegrin binding protein - useful for, e.g. treating bone diseases by modulating osteoclast differentiation and for diagnosis {\sf Constant}
Sequence
                                                                                                                                                                                                                                                                                                                                      Example 12;
                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-594578/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boyle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AMGE-) AMGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09846751-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Paget's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR hypercalcaemia; osteoclast differentiation and activation receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Osteoprotegerin binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine osteoclast differentiation and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 CKPWTNCTL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 ckpwtnctl 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
625
                                                                                                                                                                                                                                                                                                                                      Fig 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in binding protein; OPG osteoclast maturation;
                         loosening of prostheses, romote bone growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0052521.
97US-0842842.
97US-0880855.
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                                                                                                                                                                                                                                                                                                                                   47pp;
                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 binding protein; arthritis bone disease; metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activation receptor
                                         optionally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                          combination with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ODAR;
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Query Match Best Local Similarity

3.2%; 100.0%;

Score 9; 1 Pred. No.

DB 19; . 7.8;

Length 625

Query Match
Best Local Similarity
Matches 9; Conserv

Conservative

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Mismatches

Indels

0, Gaps

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3.2%; 100.0%;

Score 9; | Pred. No.

DB 7. 19;

Length 625

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AAW69958
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                                                                    CC factor-kappab (NF-kB)) polypetide which is a homolog of the human RANK. CC RANK is a member of the tumour necrosis factor (TNF) family. A soluble CC RANK may be used for inhibiting activation of NF-kB, by contacting a cell CC expressing membrane-associated RANK with a soluble RANK which binds to CC RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be used to induce maturation of dendritic cells and enhance their CC allo-stimulatory capacity, thereby augmenting an immune response. The CC soluble RANK polypeptide composition may also be used for regulating an CC immune or inflammatory response. Inhibition of NF-kB by RANK antagonists CC may be useful in ameliorating negative effects of an inflammatory creations. They can also be used in adjunct therapy for disease CC characterised by neoplastic cells that express RANK. RANKL polypeptides CC can inflammatory response, and also for protecting RANK. RANKL polypeptides CC can inflammatory response, and also for protecting RANK. RANKL polypeptides CC can inflammatory response, and also for protecting RANK. RANKL polypeptides CC can inflammatory response, and also for protecting RANK. RANKL polypeptides CC can inflammatory response, and also be used for protecting RANK. RANKL polypeptides CC can also be used in hibitors of RANK and thus inhibitors of CC can inflammatory response, and also for protecting RANK. expressing cells companies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-OCT-1997;
23-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murine NF-kB receptor activator muRANK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW69958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 14; Pages 62-64; 80pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated ligand for receptor activator of NF-kappa B \,^\circ used to develop products for augmenting an immune response for inhibiting \,^\circ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anderson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RANKL; RANK ligand; tumour necrosis factor; TNF; murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RANK; necrosis factor-kappa B; NF-kB; immune response; inflammatory response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-OCT-1998
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Sequence
                                                        screening
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DM,
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  625
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97US-0813509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for augmenting an immune response ponse and for protection of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŗ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maraskovsky
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RESULT
AAW68294
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                                                       Query Match
Best Local S
Matches
                                                                                                                                                                 This represents the murine muRANK (receptor activator of necrosis factor kappab (NF-KB)) polypetide which is a homolog of the human RANK. RANK is a member of the tumour necrosis factor (TNF) family. Host cells transformed or transfected with an expression vector comprising the RANK encoding nucleic acid can be used to produce recombinant RANK protein. The soluble RANK may be used for inhibiting activation of NF-KB, by contacting a cell expressing membrane-associated RANK with a soluble RANK which binds to RANK ligand (RANKL). The soluble RANK polypeptide composition may also be used for regulating an immune or inflammatory response. Inhibition of NF-KB by RANK antagonists may be useful in ameliorating negative effects of an inflammatory response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-cused in adjunct therapy for disease characterised by neoplastic cells that express RANK. The products can also be used for detection and drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-OCT-1997;
23-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RANK; necrosis factor-kappa B; NF-kB; receptor activator; human; immune response; inflammatory response; toxic shock; sepsis; RANKL; RANK ligand; tumour necrosis factor; TNF; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW68294 standard;
                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated receptor activator of necrosis factor-kappa B for, e.g. developing products for regulating an immune or inflammatory response, treating toxic shock or sepsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
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ckpwtnctl 178
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DB; AAV41373.
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9; Conser
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96US-0059978.
97US-0813509.
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                 Mouse; receptor; RANK; Receptor activator of NF-kappaB; osteoclast activity; immune response; inflammatory response; excess bone resorption; osteoclast generation; bone loss; osteoporosis; Paget's disease; bone cancer; cancer; hypercalcemia; osteoclastogenesis; metastasising cancer; osteoclast differentiation; signal transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence is the osteoclast formation promoting factor (OBM) binding protein (OBM-BP) of the invention. The protein is useful as a preventive and/or treating agent for bone metabolic diseases such as osteoporosis. Substances which inhibit the binding of OBM to OBM-BP can be used as biochemical reagents.
                                                                                                                                                                                                                                                                                                                                              A mouse receptor activator of NF-kappaB designated RANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \mathsf{OBM}\text{-}\mathsf{BP};\ \mathsf{OBM}\ \mathsf{binding}\ \mathsf{protein};\ \mathsf{osteoclast}\ \mathsf{formation} bone metabolic disease; osteoporosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY59509 standard; Protein; 625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A new protein, a DNA and its application
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Pred. No.
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CC in individuals inflicted with excess bone resorption. Especially, the
RANK protein is used to treat individuals at risk for excess bone loss,
CC osteoporosis, Paget's disease, bone cancer and cancers associated with
Nypercalcemia. The RANK protein ameliorates the effects of excess bone
CC loss, by binding to its ligand and inhibiting binding of other cells
CC expressing RANK. It thus decreases osteoclastogenesis when administered
CI into metastasising cancer, prostrate, hematologic, head and neck, and renal
CC melanomas, lung cancer, prostrate, hematologic, head and neck, and renal
CC which metastasise to bone and induce bone breakdown by locally disrupting
CC pathway. This results in the reduction in the osteoclast differentiation
CC pathway. This results in the reduction in the number of osteoclasts,
CC lesser bone rescorption and relief from the negative effects by
CC interfering with I/II signal transduction that leads to the
CC differentiation of osteoclasts
CC reportiation of captacolasts productors into osteoclasts
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Best Local
                                                                                                                                                  Murine; receptor activator of nuclear factor kappaB; RANK; NF; tumour necrosis factor; TNF; TNF receptor associated factor; TRAF; immune response; inflammatory response; graft-versus-host reaction; toxic shock; sepsis; acute inflammatory reaction; bone resorption; anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory
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03-DEC-1998;
Peptide
                                                                                             Mus
                                                                                                                                                                                                                                                                                                                                                Murine receptor activator of NF kappaB (RANK) protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             differentiation of osteoclast precursors into osteoclasts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regulating an immune or inflammatory response, especially to de
excess bone resorption, and for inhibiting osteoclast activity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Receptor activator of NF-kappaB). The protein is used to regulate osteoclast activity. The RANK protein or its fragments are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The
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| 170 ckpwtnctl 178
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9; Conserv
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ilarity 100.0%;
Conservative 0;
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98US-0110836
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Location/Qualifiers
1..30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 9;
Pred. No.
                                                                                                                                                     immunosuppressant; anti-inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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Qγ

Matches Query Match

Conservative

0;

100.0%; 3.28;

Score 9; 1 Pred. No. Mismatches

DB 22; o. 7.8;

Length 625; Indels

0

Gaps

0

Sequence

625 AA;

망

170 ckpwtnctl 178 141 CKPWTNCTL 149 Local Similarity les 9; Conserv

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The patent discloses novel receptor activator of nuclear factor (NF)-
CC kappab (RANK) proteins and their corresponding DNAs. RANK is a member
CC of the tumour necrosis factor (TNF) receptor superfamily and associates
CC with TNF receptor associated factor (TRAF) 2 and 3 which are important
CC in the regulation of immune and inflammatory response. The receptors
CC are useful for regulating immune response and in screening for inhibitors
CC of these receptors. The cytoplasmic domain of RANK is used in developing
CC assays for inhibit or so f signal transduction, e.g. for screening the
CC molecules that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3,
CC TRAF5 and particularly TRAF6. NF-Rappab inhibition by RANK antagonists
CC are useful in ameliorating the negative effects of an inflammatory
CC response that result from triggering of RANK, e.g. in treating toxic
CC shock or sepsis, graft-versus-host reactions, acute inflammatory
CC reactions and the effects of bone resorption. RANK acts as an anti-
CC apoptotic signal and rescue the cells that express RANK from apoptosis.
CC soluble forms of the receptor are used in vitro based
CC screening tests for agonists or antagonists of RANK activity, as
CC antagonists of RANK mediated NF-kappa B activation, or to inhibit
CC transduction of a signal via RANK. RANK compositions are used in the
CC development of both agonistic and antagonistic antibodies, or as an
CC adjunct therapy for disease characterised by neoplastic cells that
CC express RANK. Compounds that interfere with RANK/TRAF6 interactions
CC are useful for modulating the formation of osteoclast from osteoclast
CC express RANK. Composing the formation of osteoclasts from osteoclast
CC are used as inhibitors of disease sassociated with excess bone resorption
CC and as immunosuppressants or anti-inflammatory agents. The RANK DNAs are
CC are useful in preparing kits for the detection of soluble RANK, or
CC and the presence or distribution of RANK transcripts, while the proteins
CC are useful.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-DEC-1996;
07-MAR-1997;
14-OCT-1997;
23-DEC-1996;
07-MAR-1997;
22-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New receptor activator of NF-kappaB (RANK) polypeptides, useful for regulating immune response, in screening for RANK inhibitors, or as adjunct therapy for disease characterized by neoplastic cells that express RANK -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 14; Column 77-80; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
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                                         from murine.
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DB; AAD15312.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Galibert L;
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97US-0077181.
97US-0064671.
96US-0772330.
97US-0813509.
97US-0996139.
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31..625
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Best Local s
Matches 9
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07-MAR-1997;
14-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to receptor activator of NF-chi B (RANK) DNA. RANK is mapped to chromosome 18922.1 and its ligand (RANKL) to chromosome 13914. RANK and RANKL are type 1 and type 2 transmembrane. proteins respectively. RANK is a member of the tumour necrosis factor (TNF) superfamily and it closely resembles CD40 in the extracellular region. RANK associates with TNF receptor-associated factor (TRAF) 2 and TRAF3. The DNA molecules are useful for producing ligands of RANK. The ligands are useful for regulating immune response and in screening for any control of RANK. The present sequence is murine RANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
Region
  AAE01994,
                                                       AAE01994 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New DNA molecules, useful for producing ligands (which are useful for regulating immune response and in screening for inhibitors of NF-chi receptor activator of NF-chi B (RANK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-DEC-1997;
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                                                                                                                                                                                       170
                                                                                                                                                                                                                                      141 CKPWINCTL 149
                                                                                                            27
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                                                                                                                                                                                    |||||||||
| ckpwtnctl 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-407216/43.
DB; AAD08716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor activator of NF-chi B; RANK; tumour necrosis factor; NF receptor-associated factor; TRAF; ligand; immune response; ome 18q22.1; RANKL; chromosome 13q14; transmembrane protein.
                                                                                                                                                                                                                                                                                              Similarity 100.
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                 625 AA
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97US-0077181.
97US-0064671.
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                                                    Protein;
                                                                                                                                                                                                                                                                                   3.2%; >--
100.0%; Pr
                                                                                                                                                                                                                                                                                           score 9; DB 2
; Pred. No. 7.8
0; Mismatches
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                                                                                                                                                                                                                                                                                                                    DB 22;
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                                                                                                                                                                                                                                                                                                                                                Length 625;
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                                                                                                                                                                                                                                                                                              Gaps
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170 ckpwtnctl 141 CKPWINCTL Query Match
Best Local Similarity
Matches 9; Conser

Conservative

0;

Mismatches . DB .8; 0

0

Gaps

0

3.2%;

Score 9; Pred. No.

Length 625; Indels

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The present invention relates to a novel receptor, referred to as RANK CC (receptor activator of NF (nuclear factor)-kappaB), a member of TNF CC (tumour necrosis factor) receptor superfamily. RANK is a Type I CC transmembrane protein that interacts with TNF receptor-associated CC factors (TRAFS). Triggering of RANK by overexpression or co-expression CC of RANK and membrane bound RANK ligand (RANKL) results in upregulation CC of the transcription factor WF-kappaB, a ubiquitous transcription factor CC that is most extensively utilised in cells of the immune system. CC inhibition of Nf-kappaB by RANK antagonists is useful in ameliorating CC negative effects of inflammatory reactions, and the effects of excess CC bone resorption. The RANK DNAS, proteins and their analogues are useful CC for the preparation of pharmaceutical compositions, for infecting target CC cells for use in gene therapy applications in diagnosing diseases CC associated with RANK, and as targets for use in screening assays. They can be used in the treatment or diagnosis of immune system dysfunction. The present invention also encompasses gene therapy methods to correct CC gene-activating mutations, associated with e.g. familial expansile costeolysis (FEO) and early onset paget's disease of bone (EP). The CC present amino acid sequence is murine RANK (murank) protein. This CC amino acid signal sequence, a 184 amino acid extracellular domain, a 21 amino acid transmembrane domain and a 390 amino acid cytoplasmic tail.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse; receptor activator of NF-kappaB; RANK; nuclear factor-kappaB; NF-kappaB; tumour necrosis factor; TNF; type I transmembrane protein; TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopathic; inflammatory reaction; bone resorption; gene therapy; immunomodulator; immune system dysfunction; familial expansile osteolysis; FEO; early onset Paget's disease of bone; EP; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-NOV-1999;
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New DNA encoding a receptor activator of NF-kappaB polypeptide for the treatment of Paget's disease and Familial Expansile Osteolysis (FEO) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anderson DM, Hughes AE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-NOV-2000; 2000WO-US31459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-329222/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD05905
625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 80-82;
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197..214
/label- Spacer_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96pp;
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ABG01304
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AC ABGC
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AC ABGC
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XX
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KW Huma
KW Food
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AAY44302
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                                                                                                         RESULT
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Best Local (
                                                                                                                                                                      Matches
                                                                                                                                                                                                                             The present sequence is a functional mouse acrosome reaction protein, PKDREJ or P3. PKDREJ is a sperm protein involved in binding the sperm to the egg and/or triggering the acrosome reaction. It exhibits homology to human polycystin-1 and surEJ. It can be used to identify antibodies or proteins that block the acrosome reaction and compounds that trigger acrosome reaction in the absence of zona protein can be used to increase fertility and those blocking its action can be used as contraceptives. DNA encoding PKDREJ can be used gene therapy and also as primer or probe for identifying sequences that encode mutant forms of acrosome reaction protein.
                                                                      ABG01304;
                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse acrosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY44302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY44302 standard; Protein;
        Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                               Harris PC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        zona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acrosome reaction protein; P3; Polycystic Kidney Disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-FEB-2000
                                  Novel human diagnostic protein #1295.
                                                    13-FEB-2002
                                                                                       ABG01304 standard;
                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                           fertility treatment
                                                                                                                                                                                                                                                                                                                                                                  New functional mammalian acrosome reaction protein, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                (MEDI-) MEDICAL RES COUNCIL.
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|allllglgl 14
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                                                                                                                                                                      9;
                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             Hugues JR,
                                                                                                                                                                                                                 2126
                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                        2; 40pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-GB01839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   on protein; P3; sperm protein; polycystin-1; suREJ; ey Disease and Receptor for Egg Jelly protein; PKDF fertility; contraceptive; gene therapy; mouse.
                                                                                        Protein;
                                                    entry)
                                                                                                                                                                             3.2%;
                                                                                                                                                                                                                                                                                                                                        English.
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                                                                                        51
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Pred. No.
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Best Local S
Matches 8
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23-AUG-2000;
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                                                                              ABG18404;
                                                                                                                                                                                                                       Sequence
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CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome cand gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags complyucation of the combinant production of (II). The combinant production of (II). The combinant production of (II). The combination of the combination of the combination of combination of the combination of combination of the combination of combination of sites expressing (II). (I) and (II) are useful in medical combination of sites expressing (II). (I) and (II) are useful for treating combination of combination and sequences. ABG00010-ABG30377 represent novel human combination of the combinat
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Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                  ABG18404 standard; Protein;
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                                                                                                                                                           Query Match
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N-PSDB; AAS82591.
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23-AUG-2000; 2000US-0649167.
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100.0%; Pred. No. 8.1;
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